

GenCore version 5.1.6  
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protein - protein search, using sw model

on: October 27, 2004, 16:51:34 ; Search time 23.1174 Seconds  
(without alignments)  
665.548 Million cell updates/sec

tle: US-10-000-439-3  
fect score: 1260  
quence: 1 EPKSCDKTHTCPPCPAPPELL.....MHIALHNYQQRSLSPK 232

oring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

arched: 478139 seqs, 66318000 residues

tal number of hits satisfying chosen parameters: 478139

nimum DB seq length: 0  
ximum DB seq length: 2000000000  
st-processing: Minimum Match 0%  
Listing first 45 summaries

tabase : Issued Patents AA:.\*  
1: /cgn2\_6/ptodata/1/iaa/5A\_COMB.pep.\*  
2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PCTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	232	2	US-08-595-043A-50
2	1225	97.2	232	4	US-09-968-362A-26
3	1225	97.2	331	3	US-09-178-859-2
4	1225	97.2	331	4	US-09-761-413-2
5	1225	97.2	360	3	US-09-180-100-11
6	1225	97.2	371	1	US-08-236-311-7
7	1225	97.2	371	3	US-08-457-918-7
8	1225	97.2	371	4	US-10-157-408-7
9	1225	97.2	376	3	US-09-180-100-22
10	1225	97.2	396	2	US-08-784-512-3
11	1225	97.2	396	3	US-09-175-228-3
12	1225	97.2	424	5	PCT-US95-03866-12
13	1225	97.2	424	5	PCT-US95-03866-14
14	1225	97.2	437	5	PCT-US96-10043-11
15	1225	97.2	442	4	US-08-472-888A-7
16	1225	97.2	442	5	PCT-US96-10043-9
17	1225	97.2	446	3	US-08-397-411-7
18	1225	97.2	449	1	US-08-458-516-13
19	1225	97.2	459	4	US-08-157-101A-7
20	1225	97.2	467	4	US-08-030-175-41
21	1225	97.2	467	4	US-08-030-175-42
22	1225	97.2	475	4	US-09-740-002-27
23	1225	97.2	476	2	US-08-378-939-10
24	1225	97.2	476	3	US-08-487-550-4
25	1225	97.2	476	3	US-08-487-550-12
26	1225	97.2	476	4	US-09-526-098-4
27	1225	97.2	476	4	US-09-526-098-12

28	1225	97.2	476	4	US-09-383-916-4	Sequence 4, Appli
29	1225	97.2	476	4	US-09-383-916-12	Sequence 12, Appli
30	1225	97.2	478	3	US-08-487-550-8	Sequence 8, Appli
31	1225	97.2	478	4	US-09-526-098-8	Sequence 8, Appli
32	1225	97.2	478	4	US-09-383-916-8	Sequence 8, Appli
33	1225	97.2	497	4	US-09-499-846-6	Sequence 6, Appli
34	1225	97.2	525	4	US-09-499-846-4	Sequence 4, Appli
35	1225	97.2	547	4	US-09-746-359A-54	Sequence 54, Appli
36	1225	97.2	567	4	US-09-825-561A-16	Sequence 16, Appli
37	1225	97.2	571	4	US-09-746-359A-53	Sequence 53, Appli
38	1225	97.2	592	4	US-09-313-943-8	Sequence 8, Appli
39	1225	97.2	622	4	US-09-499-846-2	Sequence 2, Appli
40	1225	97.2	859	4	US-09-313-942-7	Sequence 7, Appli
41	1225	97.2	951	4	US-09-313-942-9	Sequence 9, Appli
42	1224	97.1	475	4	US-09-740-002-25	Sequence 25, Appli
43	1221	96.9	462	4	US-09-289-942A-7	Sequence 7, Appli
44	1220	96.8	254	2	US-08-284-391B-33	Sequence 33, Appli
45	1220	96.8	254	3	US-09-218-950-33	Sequence 33, Appli

ALIGNMENTS

RESULT 1  
US-08-595-043A-50  
; Sequence 50: Application US/08595043A  
; Patent No. 5935824  
; GENERAL INFORMATION:  
; APPLICANT: SGARLATO, GREGORY D.  
; TITLE OF INVENTION: PROTEIN EXPRESSION SYSTEM  
; NUMBER OF SEQUENCES: 90  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: MEDLEN & CARROLL  
; STREET: 220 MONTGOMERY STREET, SUITE 2200  
; CITY: SAN FRANCISCO  
; STATE: CALIFORNIA  
; COUNTRY: UNITED STATES OF AMERICA  
; ZIP: 94104  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent In Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/595,043A  
; FILING DATE: 31-JAN-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: CARROLL, PETER G.  
; REGISTRATION NUMBER: 32,837  
; REFERENCE/DOCKET NUMBER: SGAR-00371  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: (415) 705-8410  
; TELEFAX: (415) 397-8338  
; INFORMATION FOR SEQ ID NO: 50:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 232 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
US-08-595-043A-50

Query Match	97.2%	Score	2225	DB 2	Length	232			
Best Local Similarity	97.0%	Pred. No.	3.4e-116						
Matches	225	Conservative	3	Mismatches	4	Indels	0	Gaps	0
1	EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKDTLMISRTPEVTCVVDVSHEDPEVKF	60							
1	EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKDTLMISRTPEVTCVVDVSHEDPEVKF	60							
61	NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNMNGSKYKCKVSNKALPAPIEKT	120							
61	NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNMNGSKYKCKVSNKALPAPIEKT	120							

QY 121 ISKAKVQRPPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 Db 121 ISKAKGQRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232  
 Db 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 2  
 US-09-968-362A-26  
 ; Sequence 26, Application US/09968362A  
 ; Patent No. 6797493  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sun, Lee-Hwei K  
 ; APPLICANT: Sun, Bill  
 ; APPLICANT: Sun, Cecily R  
 ; TITLE OF INVENTION: Fc fusion proteins of human granulocyte colony-stimulating factor  
 ; TITLE OF INVENTION: increased biological activities  
 ; FILE REFERENCE: 03SUN2001  
 ; CURRENT APPLICATION NUMBER: US/09/968,362A  
 ; CURRENT FILING DATE: 2001-10-01  
 ; NUMBER OF SEQ ID NOS: 28  
 ; SOFTWARE: Patent in version 3.1  
 ; SEQ ID NO 26  
 ; LENGTH: 232  
 ; TYPE: PRT  
 ; ORGANISM: Human IgG1 Fc with native hinge, CH2 and CH3 domains  
 US-09-968-362A-26

Query Match 97.2%; Score 1225; DB 4; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 3.4e-116;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
 Db 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
 QY 61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNMMGKEYCKVSNKALPAPIEKT 120  
 Db 61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNMMGKEYCKVSNKALPAPIEKT 120  
 QY 121 ISKAKVQRPPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 Db 121 ISKAKGQRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232  
 Db 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 3  
 US-09-178-869-2  
 ; Sequence 2, Application US/09178869B  
 ; Patent No. 6197294  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tac, Weng  
 ; APPLICANT: Wong, Shou  
 ; APPLICANT: Hickey, William F  
 ; APPLICANT: Hamman, Joseph P.  
 ; APPLICANT: Baetge, E. Edward  
 ; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION  
 ; FILE REFERENCE: 17810-043  
 ; CURRENT APPLICATION NUMBER: US/09/178,869B  
 ; CURRENT FILING DATE: 1998-10-26  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 331  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-178-869-2

Query Match 97.2%; Score 1225; DB 3; Length 331;  
 Best Local Similarity 97.0%; Pred. No. 5.6e-116;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
 Db 100 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 159  
 QY 61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNMMGKEYCKVSNKALPAPIEKT 120  
 Db 160 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNMMGKEYCKVSNKALPAPIEKT 219  
 QY 121 ISKAKVQRPPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 Db 220 ISKAKGQRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 279  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232  
 Db 280 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 331

RESULT 4  
 US-09-761-413-2  
 ; Sequence 2, Application US/09761413  
 ; Patent No. 6506891  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Tac, Weng  
 ; APPLICANT: Wong, Shou  
 ; APPLICANT: Hickey, William F  
 ; APPLICANT: Hamman, Joseph P.  
 ; APPLICANT: Baetge, E. Edward  
 ; TITLE OF INVENTION: CELL SURFACE-INDUCED MACROPHAGE ACTIVATION  
 ; FILE REFERENCE: 17810-043  
 ; CURRENT APPLICATION NUMBER: US/09/761,413  
 ; CURRENT FILING DATE: 2001-01-16  
 ; PRIOR APPLICATION NUMBER: US/09/178,869  
 ; PRIOR FILING DATE: 1998-10-26  
 ; NUMBER OF SEQ ID NOS: 14  
 ; SOFTWARE: Patent in Ver. 2.0  
 ; SEQ ID NO 2  
 ; LENGTH: 331  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-09-761-413-2

Query Match 97.2%; Score 1225; DB 4; Length 331;  
 Best Local Similarity 97.0%; Pred. No. 5.6e-116;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
 Db 100 EPKSCDKTHTCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 159  
 QY 61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNMMGKEYCKVSNKALPAPIEKT 120  
 Db 160 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNMMGKEYCKVSNKALPAPIEKT 219  
 QY 121 ISKAKVQRPPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 Db 220 ISKAKGQRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 279  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232  
 Db 280 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 331

RESULT 5  
 US-09-180-100-11  
 ; Sequence 11, Application US/09180100  
 ; Patent No. 6306395  
 ; GENERAL INFORMATION:  
 ; APPLICANT: NAKAMURA, No. 6306395io

APPLICANT: NAGATA, Shigekazu  
 TITLE OF INVENTION: NOVEL Eas ANTIGEN DERIVATIVE  
 FILE REFERENCE: 1110-207P  
 CURRENT APPLICATION NUMBER: US/09/180,100  
 EARLIER FILING DATE: 1998-11-02  
 EARLIER APPLICATION NUMBER: PCT/J97/01502  
 EARLIER FILING DATE: 1997-05-01  
 NUMBER OF SEQ ID NOS: 25  
 SOFTWARE: Patent in Ver. 2.0  
 SEQ ID NO 11  
 LENGTH: 360  
 TYPE: PRT  
 ORGANISM: Homo sapiens  
 -08-180-100-11

Query Match 97.2%; Score 1225; DB 3; Length 360;  
 Best Local Similarity 97.0%; Pred. No. 6.3e-116;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 1 EPKSCDKTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 129 EPKSCDKTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 188  
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 189 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 248  
 121 ISKAKVPRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180  
 249 ISKAKGPRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 308  
 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTQKLSLSFGK 232  
 309 PVLDSGDSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTQKLSLSFGK 360

SULT 6  
 -08-236-311-7  
 Sequence 7, Application US/08236311  
 Patent No. 5565335

GENERAL INFORMATION:  
 APPLICANT: Capon, Daniel J.  
 APPLICANT: Gregory, Timothy J.  
 TITLE OF INVENTION: Adhesion Variants  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/236,311  
 FILING DATE: 02-MAY-1994  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 07/936190  
 FILING DATE: 26-AUG-1992  
 APPLICATION NUMBER: 07/842777  
 FILING DATE: 18-FEB-1992  
 APPLICATION NUMBER: 07/842777  
 FILING DATE: 18-FEB-1992  
 APPLICATION NUMBER: 07/250785  
 FILING DATE: 28-SEP-1988  
 APPLICATION NUMBER: 07/104329  
 FILING DATE: 02-OCT-1987

ATTORNEY/AGENT INFORMATION:

NAME: Hasak, Janet E.  
 REGISTRATION NUMBER: 28,616  
 REFERENCE/DOCKET NUMBER: 444P1C2  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-1896  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7169  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 371 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 US-08-236-311-7

Query Match 97.2%; Score 1225; DB 1; Length 371;  
 Best Local Similarity 97.0%; Pred. No. 6.6e-116;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 1 EPKSCDKTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 140 EPKSCDKTHCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 199  
 61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120  
 200 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 259  
 121 ISKAKVPRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180  
 260 ISKAKGPRPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 319  
 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTQKLSLSFGK 232  
 320 PVLDSGDSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYTQKLSLSFGK 371

RESULT 7

US-08-457-918-7  
 Sequence 7, Application US/08457918  
 Patent No. 6117655  
 GENERAL INFORMATION:  
 APPLICANT: Capon, Daniel J.  
 APPLICANT: Gregory, Timothy J.  
 TITLE OF INVENTION: Adhesion Variants  
 NUMBER OF SEQUENCES: 25  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Genentech, Inc.  
 STREET: 460 Point San Bruno Blvd  
 CITY: South San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94080  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: patin (Genentech)  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/457,918  
 FILING DATE: 1-JUN-1995  
 CLASSIFICATION: 435  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: 08/236311  
 FILING DATE: 02-MAY-1994  
 APPLICATION NUMBER: 07/936190  
 FILING DATE: 26-AUG-1992  
 APPLICATION NUMBER: 07/842777  
 FILING DATE: 18-FEB-1992  
 APPLICATION NUMBER: 07/250785  
 FILING DATE: 28-SEP-1988

PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/104329  
FILING DATE: 02-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0444PIC3  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 371 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
US-08-457-918-7

Query Match 97.2%; Score 1225; DB 3; Length 371;  
Best Local Similarity 97.0%; Pred. No. 6.6e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDXTHTCPCPAPPELLGSPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 140 EPKSCDXTHTCPCPAPPELLGSPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 199  
QY 61 NNYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120  
DB 200 NNYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
DB 260 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 319  
QY 181 PVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQRSLSLSPGK 232  
DB 320 PVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQRSLSLSPGK 371

RESULT 8  
US-10-157-408-7  
Sequence 7, Application US/10157408  
Patent No. 6710169  
GENERAL INFORMATION:  
APPLICANT: Capon, Daniel J.  
Gregory, Timothy J.  
TITLE OF INVENTION: Adhesion Variants  
NUMBER OF SEQUENCES: 25  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Genentech, Inc.  
STREET: 460 Point San Bruno Blvd  
CITY: South San Francisco  
STATE: California  
COUNTRY: USA  
ZIP: 94080  
COMPUTER READABLE FORM:  
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: patin (Genentech)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/10/157,408  
FILING DATE: 28-May-2002  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US/08/457,918  
FILING DATE: 1-JUN-1995  
APPLICATION NUMBER: 08/236311  
FILING DATE: 02-MAY-1994  
APPLICATION NUMBER: 07/936190  
FILING DATE: 26-AUG-1992  
APPLICATION NUMBER: 07/842777  
FILING DATE: 18-FEB-1992

APPLICATION NUMBER: 07/250785  
FILING DATE: 28-SEP-1988  
APPLICATION NUMBER: 07/104329  
FILING DATE: 02-OCT-1987  
ATTORNEY/AGENT INFORMATION:  
NAME: Kubinec, Jeffrey S.  
REGISTRATION NUMBER: 36,575  
REFERENCE/DOCKET NUMBER: P0444PIC3  
TELEPHONE: 415/225-8228  
TELEFAX: 415/952-9881  
TELEX: 910/371-7168  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 371 amino acids  
TYPE: amino acid  
TOPOLOGY: linear  
SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
US-10-157-408-7

Query Match 97.2%; Score 1225; DB 4; Length 371;  
Best Local Similarity 97.0%; Pred. No. 6.6e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDXTHTCPCPAPPELLGSPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 140 EPKSCDXTHTCPCPAPPELLGSPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 199  
QY 61 NNYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120  
DB 200 NNYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 259  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
DB 260 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 319  
QY 181 PVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQRSLSLSPGK 232  
DB 320 PVLDSGGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQRSLSLSPGK 371

RESULT 9  
US-09-180-100-22  
Sequence 22, Application US/09180100  
Patent No. 6306395  
GENERAL INFORMATION:  
APPLICANT: NAKAMURA, No. 6306395io  
Shigekazu  
APPLICANT: NAKAMURA, Shigekazu  
TITLE OF INVENTION: NOVEL Fas ANTIGEN DERIVATIVE  
FILE REFERENCE: 1110-207P  
CURRENT APPLICATION NUMBER: US/09/180,100  
CURRENT FILING DATE: 1998-11-02  
EARLIER APPLICATION NUMBER: PCT/Jp97/01502  
EARLIER FILING DATE: 1997-05-01  
NUMBER OF SEQ ID NOS: 25  
SOFTWARE: Patentin Ver. 2.0  
SEQ ID NO 22  
LENGTH: 376  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-09-180-100-22

Query Match 97.2%; Score 1225; DB 3; Length 376;  
Best Local Similarity 97.0%; Pred. No. 6.8e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDXTHTCPCPAPPELLGSPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 145 EPKSCDXTHTCPCPAPPELLGSPSVFLPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 204  
QY 61 NNYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120  
DB 205 NNYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 264

121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180  
 265 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 324  
 181 PVLDSVGSFELYSLKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232  
 325 PVLDSVGSFELYSLKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 376

SULT 10  
 -08-784-512-3  
 Sequence 3, Application US/08784512  
 Patent No. 5872209  
 GENERAL INFORMATION:  
 APPLICANT: BARTNIK, Eckart  
 APPLICANT: EIDENMUELLER, Bernd  
 APPLICANT: BUETTNER, Frank  
 APPLICANT: CATERSON, Bruce  
 APPLICANT: HUGHES, Clare  
 TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)  
 TITLE OF INVENTION: and native aggregran to study the proteolytic activity of  
 TITLE OF INVENTION: "Aggregranase" in cell culture systems  
 NUMBER OF SEQUENCES: 4  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Foley & Lardner  
 STREET: Suite 500, 3000 K Street, N.W.  
 CITY: Washington, D.C.  
 COUNTRY: USA  
 ZIP: 20007-5109  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk  
 COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: Patentin Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA:  
 APPLICATION NUMBER: US/08/784,512  
 FILING DATE: 17-JAN-1997  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: EP 96100682.2  
 FILING DATE: 18-JAN-1996  
 ATTORNEY/AGENT INFORMATION:  
 NAME: GRANADOS, Patricia D.  
 REGISTRATION NUMBER: 33,683  
 REFERENCE/DOCKET NUMBER: 18748/311  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (202)672-5300  
 TELEFAX: (202)672-5399  
 TELEX: 904136  
 INFORMATION FOR SEQ ID NO: 3:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 396 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: protein  
 FEATURE:  
 NAME/KEY: Protein  
 LOCATION: 1..396  
 3-08-784-512-3

Query Match 97.2%; Score 1225; DB 2; Length 396;  
 Best Local Similarity 97.0%; Pred. No. 7.3e-116;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Y 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 b 165 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 224  
 Y 61 NNYVDGVEVHNKTRPEEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120  
 b 225 NNYVDGVEVHNKTRPEEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 284

QY 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 180  
 Db 285 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPP 344  
 QY 181 PVLDSVGSFELYSLKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232  
 Db 345 PVLDSVGSFELYSLKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 396

RESULT 11  
 US-09-176-228-3  
 ; Sequence 3, Application US/09176228  
 ; Patent No. 6180334  
 ; GENERAL INFORMATION:  
 ; APPLICANT: BARTNIK, Eckart  
 ; APPLICANT: EIDENMUELLER, Bernd  
 ; APPLICANT: BUETTNER, Frank  
 ; APPLICANT: CATERSON, Bruce  
 ; APPLICANT: HUGHES, Clare  
 ; TITLE OF INVENTION: An artificial recombinant substrate (rAGG 1)  
 ; TITLE OF INVENTION: and native aggregran to study the proteolytic activity of  
 ; TITLE OF INVENTION: "Aggregranase" in cell culture systems  
 ; NUMBER OF SEQUENCES: 4  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Foley & Lardner  
 ; STREET: Suite 500, 3000 K Street, N.W.  
 ; CITY: Washington, D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20007-5109  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.25  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/09/176,228  
 ; FILING DATE:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/784,512  
 ; FILING DATE: 17-JAN-1997  
 ; APPLICATION NUMBER: EP 96100682.2  
 ; FILING DATE: 18-JAN-1996  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: GRANADOS, Patricia D.  
 ; REGISTRATION NUMBER: 33,683  
 ; REFERENCE/DOCKET NUMBER: 18748/311  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: (202)672-5300  
 ; TELEFAX: (202)672-5399  
 ; TELEX: 904136  
 ; INFORMATION FOR SEQ ID NO: 3:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 396 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; FEATURE:  
 ; NAME/KEY: Protein  
 ; LOCATION: 1..396  
 ; US-09-176-228-3

Query Match 97.2%; Score 1225; DB 3; Length 396;  
 Best Local Similarity 97.0%; Pred. No. 7.3e-116;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 Db 165 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKF 224  
 QY 61 NNYVDGVEVHNKTRPEEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120  
 Db 225 NNYVDGVEVHNKTRPEEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 284

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180  
 DB 285 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 344  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVWHEALHNYHQORSLSLSPGK 232  
 DB 345 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVWHEALHNYHQORSLSLSPGK 396

RESULT 12

PCT-US95-03866-12  
 ; Sequence 12, Application PC/TUS9503866  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CytoMed, Inc. (all states except US)  
 ; APPLICANT: Nocka, Karl (US only)  
 ; APPLICANT: Lobell, Robert B (US only)  
 ; TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND  
 ; TITLE OF INVENTION: FLT-3/FLK-2 LIGAND  
 ; NUMBER OF SEQUENCES: 36  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Neave  
 ; STREET: 1251 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: United States of America  
 ; ZIP: 10020  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/03866  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/220,379  
 ; FILING DATE: 28-MAR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Haley Jr, James F  
 ; REGISTRATION NUMBER: 27,794  
 ; REFERENCE/DOCKET NUMBER: CytoMed/2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-596-9000  
 ; TELEFAX: 212-596-9090  
 ; INFORMATION FOR SEQ ID NO: 12:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 424 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; PCT-US95-03866-12

Query Match 97.2%; Score 1225; DB 5; Length 424;  
 Best Local Similarity 97.0%; Pred. No. 8e-116;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCPPCPAPELLGPPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 DB 193 EPKSCDKTHTCPPCPAPELLGPPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 252  
 QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120  
 DB 253 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 312  
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180  
 DB 313 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 372  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVWHEALHNYHQORSLSLSPGK 232  
 DB 373 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVWHEALHNYHQORSLSLSPGK 424

RESULT 13

PCT-US95-03866-14  
 ; Sequence 14, Application PC/TUS9503866  
 ; GENERAL INFORMATION:  
 ; APPLICANT: CytoMed, Inc. (all states except US)  
 ; APPLICANT: Nocka, Karl (US only)  
 ; APPLICANT: Lobell, Robert B (US only)  
 ; TITLE OF INVENTION: STABILIZED DIMER OF KIT LIGAND AND  
 ; TITLE OF INVENTION: FLT-3/FLK-2 LIGAND  
 ; NUMBER OF SEQUENCES: 36  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Fish & Neave  
 ; STREET: 1251 Avenue of the Americas  
 ; CITY: New York  
 ; STATE: New York  
 ; COUNTRY: United States of America  
 ; ZIP: 10020  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US95/03866  
 ; FILING DATE:  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: US 08/220,379  
 ; FILING DATE: 28-MAR-1994  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Haley Jr, James F  
 ; REGISTRATION NUMBER: 27,794  
 ; REFERENCE/DOCKET NUMBER: CytoMed/2  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 212-596-9000  
 ; TELEFAX: 212-596-9090  
 ; INFORMATION FOR SEQ ID NO: 14:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 424 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; PCT-US95-03866-14

Query Match 97.2%; Score 1225; DB 5; Length 424;  
 Best Local Similarity 97.0%; Pred. No. 8e-116;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCPPCPAPELLGPPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 DB 193 EPKSCDKTHTCPPCPAPELLGPPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 252  
 QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120  
 DB 253 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 312  
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 180  
 DB 313 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVWESNGQPENNYKTTTP 372  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVWHEALHNYHQORSLSLSPGK 232  
 DB 373 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVWHEALHNYHQORSLSLSPGK 424

RESULT 14

PCT-US96-10043-11  
 ; Sequence 11, Application PC/TUS9610043  
 ; GENERAL INFORMATION:  
 ; APPLICANT: The General Hospital Corporation  
 ; TITLE OF INVENTION: P-SELECTIN LIGANDS AND RELATED MOLECULES

Thu Oct 28 05:36:47 2004

TITLE OF INVENTION: AND METHODS  
NUMBER OF SEQUENCES: 14  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Fish & Richardson P.C.  
STREET: 225 Franklin Street  
CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02210-2804  
COMPUTER READABLE FORM: disk  
MEDIUM TYPE: floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.30  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: PCT/US96/10043  
FILING DATE:  
CLASSIFICATION:  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 60/000,213  
FILING DATE: 14-JUN-1995  
CLASSIFICATION:  
ATTORNEY/AGENT INFORMATION:  
NAME: Lech, Karen F.  
REGISTRATION NUMBER:  
REFERENCE/DOCKET NUMBER: 00786/284001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617/542-5070  
TELEFAX: 617/542-8906  
TELEX: 200154  
INFORMATION FOR SEQ ID NO: 11:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 437 amino acids  
TYPE: amino acid  
STRANDEDNESS: not relevant  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
T-US96-10043-11

CITY: Boston  
STATE: MA  
COUNTRY: USA  
ZIP: 02110  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible  
OPERATING SYSTEM: DOS  
SOFTWARE: FastSeq for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/472,888A  
FILING DATE: 07-JUN-1995  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 07/618,314  
FILING DATE: 23-NOV-1990  
ATTORNEY/AGENT INFORMATION:  
NAME: Elbing, Karen L.  
REGISTRATION NUMBER: 35,238  
REFERENCE/DOCKET NUMBER: 00786/258001  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 617-428-0200  
TELEFAX: 617-428-7045  
TELEX:  
INFORMATION FOR SEQ ID NO: 7:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 442 amino acids  
TYPE: amino acid  
STRANDEDNESS: unknown  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-472-888A-7

Query Match 97.2%; Score 1225; DB 4; Length 442;  
Best Local Similarity 97.0%; Pred. No. 8.5e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 211 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 270  
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWNGKEYKCKVSNKALPAPIEKT 120  
DB 271 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDLNGLKEYKCKVSNKALPAPIEKT 330  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
DB 331 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 390  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQRSLSLSPGK 232  
DB 391 PVLDSGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKLSLSFGK 442

Search completed: October 27, 2004, 17:05:53  
Job time : 24.1174 secs

RESULT 15  
3-08-472-888A-7  
Sequence 7, Application US/08472888A  
Patent No. 6613746  
GENERAL INFORMATION:  
APPLICANT: Seed, Brian  
APPLICANT: Walz, Gerd  
TITLE OF INVENTION: AGP-ANTIBODY FUSION PROTEINS  
TITLE OF INVENTION: AND RELATED MOLECULES AND METHODS  
NUMBER OF SEQUENCES: 9  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Clark & Elbing LLP  
STREET: 176 Federal Street

Query Match 97.2%; Score 1225; DB 5; Length 437;  
Best Local Similarity 97.0%; Pred. No. 8.4e-116;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 206 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 265  
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWNGKEYKCKVSNKALPAPIEKT 120  
DB 266 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDLNGLKEYKCKVSNKALPAPIEKT 325  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
DB 326 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 385  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQRSLSLSPGK 232  
DB 386 PVLDSGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHTQKLSLSFGK 437

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1 protein - protein search, using sw model

on: October 27, 2004, 16:51:09 ; Search time 28.7722 Seconds  
(without alignments)  
1103.547 Million cell updates/sec

itle: US-10-000-439-2

erfect score: 1764

equence: 1 ASTKGPSVFPLAPSGKSTG.....MHEALNHYQORSLSPGK 330

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 283416 seqs, 96216763 residues

total number of hits satisfying chosen parameters: 283416

imum DB seq length: 0

aximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase :

PIR 79: \*  
1: PIR1: \*  
2: PIR2: \*  
3: PIR3: \*  
4: PIR4: \*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

result No.	Query Match	Score	Length	ID	Description
1	1729	98.0	330	1 GHU	Ig gamma-1 chain C
2	1592.5	90.3	377	2 A23511	Ig gamma-3 chain C
3	1590.5	90.2	377	2 A60764	Ig gamma-3 chain C
4	1566	88.8	326	1 G2HU	Ig gamma-2 chain C
5	1552.5	88.0	327	1 G4HU	Ig gamma-4 chain C
6	1225.5	69.5	374	2 S69339	Ig heavy chain v r
7	1225	69.4	328	2 I47159	Ig gamma 2a chain
8	1222	69.3	255	4 S31866	Ig gamma-1 chain C
9	1219	69.1	328	2 I47160	Ig gamma 2b chain
10	1216	68.9	234	2 PT0207	Ig gamma chain C r
11	1193	67.6	328	2 I47158	Ig gamma 1 chain c
12	1192.5	67.6	323	1 GHRB	Ig gamma chain C r
13	1189	67.4	328	2 I47161	Ig gamma 3 chain c
14	1174.5	66.6	329	1 G2GP	Ig gamma-1 chain C
15	1163.5	66.0	472	2 S31459	Ig gamma-1 chain -
16	1144.5	64.9	470	2 S22080	Ig heavy chain pre
17	1125.5	63.8	308	2 C30554	Ig heavy chain C r
18	1123	63.7	289	1 G3RUWI	Ig gamma-3 heavy c
19	1117.5	63.4	333	2 PS0018	Ig gamma-2b chain
20	1116	63.3	444	2 C4436	monoclonal antibod
21	1114	63.2	326	2 PS0017	Ig gamma-1 chain C
22	1109	62.9	324	1 G1MS	Ig gamma-1 chain C
23	1108	62.8	329	1 G3MSC	Ig gamma-3 chain C
24	1104	62.6	393	1 G3MSM	Ig gamma-1 chain C
25	1097	62.2	398	1 G3MSM	Ig gamma-3 chain C
26	1093	62.0	330	1 G2NSA	Ig gamma-2a chain
27	1093	62.0	469	2 S37483	Ig gamma-2a chain
28	1090.5	61.8	335	1 G2NSAB	Ig gamma-2a chain
29	1088	61.7	399	1 G2NSAM	Ig gamma-2a chain

## ALIGNMENTS

### RESULT 1

GHU

Ig gamma-1 chain C region - human

C:Species: Homo sapiens (man)

C:Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C:Accession: A93433; S36861; S33887; B90563; A90564; B91568; A91723; A02146

R:Ellison, J.W.; Berson, B.J.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A/Reference number: A93433; MUID:62274238; PMID:6287432

A/Accession: A93433

A/Molecule type: DNA

A/Residues: 1-330 <ELL>

A/Cross-references: UNIPROT:P01857; EMBL:Z17370

A/Note: this sequence has the Gm(17) allotypic marker, 97-Lys, and the Gm(1) markers, 2

A/Note: Lys-330 is removed after translation

R:Harris, L.J.

submitted to the EMBL Data Library, October 1992

A/Reference number: S33904

A/Accession: S36861

A/Molecule type: DNA

A/Residues: 2-330 <HAR>

A/Cross-references: EMBL:Z17370

R:Takahashi, N.; Ueda, S.; Obata, M.; Nikaide, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a s

A/Reference number: S33887; MUID:83001943; PMID:6811139

A/Accession: S33887

A/Molecule type: DNA

A/Residues: 88-113;235-330 <TAX>

A/Cross-references: EMBL:Z17370

R:Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C

Biochemistry 9, 3161-3170, 1970

A/Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequen

A/Reference number: A90563; MUID:71064024; PMID:5489771

A/Contents: myeloma protein Eu

A/Accession: B90563

A/Molecule type: protein

A/Residues: 1-96, 'R', 98-135 <CUN>

A/Note: this sequence has the Gm(3) marker, 97-Arg

R:Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A/Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer

A/Reference number: A90564; MUID:71064025; PMID:5530842

A/Contents: Eu

A/Accession: A90564

A/Molecule type: protein

A/Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, 'R; Ponstingl, H.; Hilschmann, N.

A/Note: this sequence has the Gm(non-1) markers, 239-Glu and 241-Met

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A/Title: Die Primaerstruktur eines monoklonalen IgG1-immunglobulins (Myelomprotein Nie),



20-85/Domain: immunoglobulin homology <IMM>

```
Query Match      90.2%; Score 1590.5; DB 2; Length 377;
Best Local Similarity 80.1%; Pred. No. 1.1e-102;
Matches 302; Conservative 13; Mismatches 15; Indels 47; Gaps 1;

1 ASTKGPSVFPLAPSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
1 ASTKGPSVFPLAPCSRSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60

61 GLYSLSVVTVPPSSSLGTQTVICNVNHPKNTKVDKKV----- 98
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
61 GLYSLSVVTVPPSSSLGTQTVICNVNHPKNTKVDKKVKTPLGDTHTTCPCPEPKSC 120

99 -----EPKSCDKTHTCPPCPAPPELLGGPSVFLPPPKPKDT 133
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121 DTPPPCPKPEKSCDTPPCPCPEPKSCDTPPCPCPEPELLGGPSVFLPPPKPKDT 180

134 LMSITPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNKTKPREEOYNSTRYVSVLTVLH 193
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
181 LMSITPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNNKTKPREEQYNSTRYVSVLTVLH 240

194 QNMNGKEYCKVSKNKAALPAPIETKISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVK 253
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
241 QDMNGKEYCKVSKNKAALPAPIETKISKAKVQPREPOVYTLPPSRDEWTKNQVSLTCLVK 300

254 GYPSDIAVEWESNGQPENNYKTPPVLDSDVGSGFLYSKLTVDKSRWQQGNVSCSVMHE 313
|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
301 GYPSDIAVEWESNGQPENNYKTPPVLDSDVGSGFLYSKLTVDKSRWQQGNVSCSVMHE 360

314 ALHNHYQORSLSLSPGK 330
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361 ALHNRYTKSLSLSPGK 377

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A:Accession: A93132

A:Molecule type: protein

A:Residues: 238-275 <HOF>

R:Hofmann, T.; Parr, D.M.

submitted to the Atlas, March 1980

A:Reference number: A94591

A:Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A:Note: the revised sequence differs from that shown in having 60-Ala and in the amidatic  
ned

R:Milstein, C.; Frangione, B.

Biochem. J. 121, 217-225, 1971

A:Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.

A:Reference number: A90553; MUID:72033500; PMID:4940472

A:Contents: annotation; myeloma protein Sa, disulfide bonds

R:Frangione, B.; Milstein, C.; Pink, J.R.L.

Nature 221, 145-148, 1969

A:Title: Structural studies of immunoglobulin G.

A:Reference number: A93157; MUID:69064124; PMID:5782707

A:Contents: annotation; Sa, disulfide bonds

C:Genetics: GDB:IGHG2

A:Gene: GDB:IGHG2

A:Cross-references: GDB:119338; OMIM:147110

A:Map position: 14q32.33-14q32.33

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kappa)  
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la;

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IM1>

F:133-202/Domain: immunoglobulin homology <IM2>

F:239-306/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83,140-200,246-304/Disulfide bonds: #status experimental

F:102,103,106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:176/Binding site: carbohydrate (Asn) (covalent) #status predicted

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A:Reference number: A90933; MUID:83157104; PMID:6299662

A:Accession: A90933

A:Molecule type: DNA

A:Residues: 1-327 <ELL>

A:Cross-references: UNIPROT:P01861

A>Note: the sequence was determined from the germline gene

R:Pink, J.R.L.; Buttery, S.H.; De Vries, G.M.; Milstein, C.

Biochem. J. 117, 33-47, 1970

A:Title: Human immunoglobulin subclasses. Partial amino acid sequence of the constant

A:Reference number: A90249; MUID:70207560; PMID:4192699

A:Accession: A90249

A:Molecule type: protein

A:Residues: 1-30; 81-326 <PIN>

C:Genetics:

A:Gene: GDB:IGHG4

A:Cross-references: GDB:119340; OMIM:147130

A:Map position: 14q32.33-14q32.33

A:Introns: 99/1; 111/1; 221/1

C:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap

tain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into la

C:Superfamily: immunoglobulin C region; immunoglobulin homology

C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin

F:20-85/Domain: immunoglobulin homology <IMI>

F:99-110/Region: hinge

F:134-203/Domain: immunoglobulin homology <IM2>

F:240-307/Domain: immunoglobulin homology <IM3>

F:14/Disulfide bonds: interchain (to light chain) #status experimental

F:27-83,141-201,247-305/Disulfide bonds: #status predicted

F:106,109/Disulfide bonds: interchain (to heavy chain) #status experimental

F:177/Binding site: carbonyl (Asn) (covalent) #status predicted

Query Match 88.0%; Score 1552.5; DB 1; Length 327;

Best Local Similarity 88.8%; Pred. No. 3.8e-100;

Matches 293; Conservative 15; Mismatches 19; Indels 3; Gaps 1;

QY 1 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHPFPAVLQSS 60

DB 1 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHPFPAVLQSS 60

QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKNTKDKKVPKSCDKTHTCPCPAPPELLGG 120

DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKNTKDKKVPKSCDKTHTCPCPAPPELLGG 117

QY 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPREEQYN 180

DB 118 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPREEQYN 177

QY 181 STYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

DB 178 STYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSQEE 237

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 300

DB 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 297

QY 301 QQGNVFCSCVMHEALHNHYQKLSLSLSPGK 330

DB 298 QQGNVFCSCVMHEALHNHYQKLSLSLSPGK 327

Query Match 88.0%; Score 1552.5; DB 1; Length 327;

Best Local Similarity 88.8%; Pred. No. 3.8e-100;

Matches 293; Conservative 15; Mismatches 19; Indels 3; Gaps 1;

QY 1 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHPFPAVLQSS 60

DB 1 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHPFPAVLQSS 60

QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKNTKDKKVPKSCDKTHTCPCPAPPELLGG 120

DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKNTKDKKVPKSCDKTHTCPCPAPPELLGG 116

QY 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPREEQYN 180

DB 116 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPREEQYN 176

QY 181 STYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

DB 178 STYRVSVLTVLHQNMMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSQEE 237

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 300

DB 238 MTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 297

QY 301 QQGNVFCSCVMHEALHNHYQKLSLSLSPGK 330

DB 298 QQGNVFCSCVMHEALHNHYQKLSLSLSPGK 327

A:Residues: 1-374 <KHA>

A:Cross-references: EMBL:X81695

R:Khamilichi, A.A.

submitted to the EMBL Data Library, September 1994

A:Reference number: S72664

A:Accession: S72664

A:Molecule type: mRNA

A:Residues: 1-140, 'C', 142-374 <KH2>

A:Cross-references: EMBL:X81695

C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 69.5%; Score 1225.5; DB 2; Length 374;

Best Local Similarity 87.1%; Pred. No. 1.8e-77;

Matches 230; Conservative 6; Mismatches 17; Indels 11; Gaps 2;

QY 78 TOTYICNVN-----HK-PSNTKYDKKVPKSCDKTHTCPCPAPPELLGSPVFLF 126

DB 111 TATYCYGYSVEGQYGRFHSQGQGLTVTSSEPKSCDKTHTCPCPAPPELLGSPVFLF 170

QY 127 PPXPCKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPREEQYNSTYRW 186

DB 171 PPXPCKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPREEQYNSTYRW 230

QY 187 SVLTVLHQNMMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQV 246

DB 231 SVLTVLHQNMMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDELTKNQV 290

QY 247 SLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRWQGNVNF 306

DB 291 SLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRWQGNVNF 350

QY 307 SC5WHEALHNHYQKLSLSLSPGK 330

DB 351 SC5WHEALHNHYQKLSLSLSPGK 374

RESULT 7

147159

Ig gamma 2a chain constant region - pig (fragment)

C:Species: Sus scrofa domestica (domestic pig)

C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000

C:Accession: I47159

R:Kaczkovics, I.; Sun, J.; Butler, J.E.

J. Immunol. 153, 3565-3573, 1994

A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a

A:Reference number: I47158; MUID:95015845; PMID:7930579

A:Accession: I47159

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-328 <KAC>

A:Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124

C:Genetics:

A:Gene: IgG2a

C:Superfamily: immunoglobulin C region; immunoglobulin homology

F:133-202/Domain: immunoglobulin homology <IMM>

Query Match 69.4%; Score 1225; DB 2; Length 328;

Best Local Similarity 67.5%; Pred. No. 1.7e-77;

Matches 224; Conservative 46; Mismatches 56; Indels 6; Gaps 2;

QY 1 ASTKGPSVFPPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHPFPAVLQSS 60

DB 1 APKTAFSVYFLAPCSRDTSGPNVALGCLASSYFPEPTVTVNSGALSSGVHTFPVLQPS 60

QY 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKNTKDKKVPKSCDKTHTCPCPAPPELLGG 120

DB 61 GLYSLSVVTVPSSSLGTQTYICNVNHPKNTKDKKVPKSCDKTHTCPCPAPPELLGG 116

QY 121 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPREEQYN 180

DB 117 PSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPREEQYN 176

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RESULT 11
I47158
Ig gamma 1 chain constant region - pig (fragment)
C/Species: Sus scrofa domestica (domestic pig)
C/Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 21-Jan-2000
C/Accession: I47158

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R;Kacskovics, I.; Sun, J.; Butler, J.E.  
 J. Immunol. 153, 3565-3573, 1994  
 A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
 A;Reference number: I47158; MUID:95015845; PMID:7930579  
 A;Accession: I47158  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-328 <KAC>  
 A;Cross-references: EMBL:U03778; NID:9433121; PIDN:AAA52216.1; PID:9433122  
 C;Genetics:  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 F;133-202/Domain: immunoglobulin homology <IMM>

Query Match 67.6%; Score 1193; DB 2; Length 328;  
 Best Local Similarity 67.2%; Pred. No. 2.7e-75;  
 Matches 223; Conservative 42; Mismatches 61; Indels 6; Gaps 3;

QY 1 ASTKPSVFLPAPSKSTSGTAAALGCLVKDYFPPEVTVSWNSGALTSGVHTFPVAVLQSS 60  
 Db 1 AKPTAPSYIPLAPCGRDVSGFVALGCLASSYFPEPVTVTWNSGALTSGVHTFPVAVLQPS 60

QY 61 GLYSLSSVTVFPSSSLGTQYICNVNHPKSNITKVDKVEPKSCDKTHTCPPCPAPPELGG 120  
 Db 61 GLYSLSSVTVFPASSLSKSYTCNVNHPATTKVDKRV--GIHQQTCTPCPGCE-VAG 116

QY 121 PSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNVKTKPREQYN 180  
 Db 117 PSVFLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNVKTKPREQYN 176

QY 181 STYKWSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPRDE 240  
 Db 177 STYKWSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPRABE 236

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTPPPVLDVSGSFYFLSKLTVDKS 298  
 Db 237 LRSKVTLTCLVIGFYPPDIHVEWESNGQPEPENTYRTTPQQDVGDFYFLSKLAVDKA 296

QY 299 RWQGNVFSVMHEALHNNHYQQRSLSPGK 330  
 Db 297 RWDGDKFECAVMHEALHNNHYTKSISKTQSK 328

RESULT 12

IG gamma chain C region - rabbit  
 C;Species: Oryctolagus cuniculus (domestic rabbit)  
 C;Date: 24-Apr-1984 #sequence\_revision 15-Nov-1984 #text change 09-Jul-2004  
 A;Accession: A91749; A90290; A93928; A90245; A94416; A02161  
 R;Bernstein, K.E.; Alexander, C.B.; Mage, R.G.  
 Immunogenetics 18, 387-397, 1983  
 A;Title: Nucleotide sequence of a rabbit IgG heavy chain from the recombinant F-I haplot  
 A;Reference number: A91749; MUID:84030930; PMID:6313520  
 A;Accession: A91749  
 A;Molecule type: mRNA  
 A;Residues: 1-323 <BER>  
 A;Cross-references: UNIPROT:P01870  
 A;Note: this sequence has the d12 allotypic marker, 104-Thr., and the e14 marker, 185-Thr  
 R;Pratt, D.M.; Mole, L.E.  
 Biochem. J. 151, 337-349, 1975  
 A;Title: Sequence studies on the constant region of the Fd sections of rabbit immunoglob  
 A;Reference number: A90290; MUID:76135469; PMID:1243651  
 A;Accession: A90290  
 A;Molecule type: protein  
 A;Residues: 1-47,'E',49-71,'pv',72-128 <PRA>  
 R;Martens, C.L.; Moore, K.W.; Steinmetz, M.; Hood, L.; Knight, K.L.  
 Proc. Natl. Acad. Sci. U.S.A. 79, 6018-6022, 1982  
 A;Title: Heavy chain genes of rabbit IgG; isolation of a cDNA encoding gamma heavy chain  
 A;Reference number: A93928; MUID:83299917; PMID:6193512  
 A;Accession: A93928  
 A;Molecule type: mRNA  
 A;Residues: 88-103,'M',105-143,'E',145-184,'A',186,'E',188-266 <MAR>  
 A;Cross-references: GB:M16426; NID:G165111; PIDN:AAA31289.1; PID:G165112

A;Note: this sequence has the d11 allotypic marker, 104-Met, and the e15 allotypic mark  
 R;Fruchter, R.G.; Jackson, S.A.; Mole, L.E.; Porter, R.R.  
 Biochem. J. 116, 249-259, 1970  
 A;Title: Sequence studies of the Fd section of the heavy chain of rabbit immunoglobulin  
 A;Reference number: A90245; MUID:70110015; PMID:5461106  
 A;Accession: A90245  
 A;Molecule type: protein  
 A;Residues: 132-143,'E',145-161 <FRU>  
 R;Hill, R.L.; Lebovitz, H.B.; Fellows Jr., R.E.; Delaney, R.  
 in Gamma Globulins, Nobel Symp. 3, Killander, J., ed., pp.109-127, Almquist and Wiksell  
 A;Reference number: A94416  
 A;Accession: A94416  
 A;Molecule type: protein  
 A;Residues: 139-151,155-172,'D',174-184,'A',186,'E',188-200,'D',202-217,'E',219-232,'Q'  
 A;Note: this has the e15 allotypic marker, 188-Ala  
 C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (ka  
 hain disulfide bonds. In some cases, such as IgA and IgG, the subunits associate into li  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 C;Keywords: Duplication; glycoprotein; heterotetramer; immunoglobulin  
 F;130-199/Domain: immunoglobulin homology <IM1>  
 F;236-303/Domain: immunoglobulin homology <IM3>  
 F;173/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 67.6%; Score 1192.5; DB 1; Length 323;  
 Best Local Similarity 67.9%; Pred. No. 2.9e-75;  
 Matches 222; Conservative 37; Mismatches 61; Indels 7; Gaps 2;

QY 4 KGPSVFLPAPSKSTSGTAAALGCLVKDYFPPEVTVSWNSGALTSGVHTFPVAVLQSSGLY 63  
 Db 4 KAPSVFLPAPCGCDTPSTVTLLGCLVKGYLPEPVTVTWNSGTLTNGVTRTFPSVQSSGLY 63

QY 64 SLSSVTVFPSSSLGTQYICNVNHPKSNITKVDKVEPKSCDKTHTCPPCPAPPELGGPSV 123  
 Db 64 SLSSVTVFPSS--QPVTNCNVNHPATNTKVDKTVAPSTCK---PTCPPELGGPSV 116

QY 124 FLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNVKTKPREQYNSTY 183  
 Db 117 FLFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNVKTKPREQYNSTI 176

QY 184 RVSVSLTCLVKGFYPSDIAVEWESNGQPKVSNKALPAPIEKTISKAKVQPREPOVYTLPPRDESLTK 243  
 Db 177 RVSVSLTCLVKGFYPSDIAVEWESNGQPKVSNKALPAPIEKTISKAKVQPREPOVYTLPPRDESLSS 236

QY 244 NQVSLTCLVKGFYPSDIAVEWESNGQPKVSNKALPAPIEKTISKAKVQPREPOVYTLPPRDESLSS 303  
 Db 237 RSVSLTCLVKGFYPSDIAVEWESNGQPKVSNKALPAPIEKTISKAKVQPREPOVYTLPPRDESLSS 296

QY 304 NVFSCVSMHEALHNNHYQQRSLSPGK 330  
 Db 297 DVFTCSVMHEALHNNHYTKSISRSFGK 323

RESULT 13

I47161  
 IG gamma 3 chain constant region - pig (fragment)  
 C;Species: Sus scrofa domestica (domestic pig)  
 C;Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
 C;Accession: I47161  
 R;Kacskovics, I.; Sun, J.; Butler, J.E.  
 J. Immunol. 153, 3565-3573, 1994  
 A;Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a s  
 A;Reference number: I47158; MUID:95015845; PMID:7930579  
 A;Accession: I47161  
 A;Status: preliminary; translated from GB/EMBL/DBJ  
 A;Molecule type: mRNA  
 A;Residues: 1-328 <KAC>  
 A;Cross-references: EMBL:U03781; NID:9433127; PIDN:AAA52219.1; PID:9433128  
 C;Genetics:  
 C;Superfamily: immunoglobulin C region; immunoglobulin homology  
 F;133-202/Domain: immunoglobulin homology <IMM>



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Db 202 GLYSLSSVTVTPASTSGAQTFICNVAPASSTKVDRKVEFGCPDCKHC-RCPPPELPGG 260
QY 121 PSVLEFPKPKDMLISRTPEVTCVVVDVSHEDPEVKENNYVDGVEVHNKTKPRREQYN 180
Db 261 PSVFIFFPKPKDMLISRTPEVTCVVVDVSHEDPEVKENNYVDGVEVHNKTKPRREQYN 320
QY 181 STYRVVSVLTVLHONMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 321 STPRVVSALPIQHDWTGKKEFKCKVHNEALPAPIVTRTISRTKGGQAREEQVYVLA 380
QY 241 LTRKQVSLTCLVKGFPYSDIAVEWESNGQP--ENNYKTTTPVLDSVGSFFLYSKLTVDKS 298
Db 381 LSKSTLSVTLCLVKGFPYSDIAVEWESNGQP--ENNYKTTTPVLDSVGSFFLYSKLTVDKS 440
QY 299 RWQOCNVFSCVMHEALHNYQORSLSLSPGK 330
Db 441 SWQEGDTYACVWHEALHNYTQKSIKPPGK 472

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Search completed: October 27, 2004, 17:04:50  
 Job time : 30.2722 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

1 protein - protein search, using sw model

in on: October 27, 2004, 16:32:53 ; Search time 149.733 Seconds  
(without alignments)  
1268.081 Million cell updates/sec

tle: US-10-000-439-2

fect score: 1764

quence: 1 ASTKGPSVFLPSSKSTSG.....MHEALHNYQQRSLSPCK 330

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 1825181 seqs, 575374646 residues

tal number of hits satisfying chosen parameters: 1825181

imum DB seq length: 0

iximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase : UniProt\_02.\*

1: uniprot\_sprot.\*

2: uniprot\_trenbl.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1729	98.0	330	1 GCI_HUMAN	P01857 homo sapien
2	1729	98.0	407	2 BAC85237	Bac85237 homo sapi
3	1729	98.0	464	2 AAH19337	Aah19337 homo sapi
4	1729	98.0	465	2 Q6GMX6	Q6gmX6 homo sapien
5	1729	98.0	466	2 AAH64496	Aah64496 homo sapi
6	1729	98.0	467	2 BAC85173	Bac85173 homo sapi
7	1729	98.0	468	2 BAC85175	Bac85175 homo sapi
8	1729	98.0	468	2 BAC85444	Bac85444 homo sapi
9	1729	98.0	469	2 Q7Z7P5	Q7z7P5 homo sapien
10	1729	98.0	470	2 Q6PJA4	Q6pja4 homo sapien
11	1729	98.0	470	2 Q7Z5W1	Q7z5W1 homo sapien
12	1729	98.0	470	2 BAC85235	Bac85235 homo sapi
13	1729	98.0	470	2 BAC85387	Bac85387 homo sapi
14	1729	98.0	470	2 AAH62336	Aah62336 homo sapi
15	1729	98.0	470	2 AAH14258	Aah14258 homo sapi
16	1729	98.0	470	2 AAH18747	Aah18747 homo sapi
17	1729	98.0	470	2 AAH25314	Aah25314 homo sapi
18	1729	98.0	471	2 BAC85388	Bac85388 homo sapi
19	1729	98.0	471	2 AAH24289	Aah24289 homo sapi
20	1729	98.0	472	2 BAC85232	Bac85232 homo sapi
21	1729	98.0	472	2 BAC86225	Bac86225 homo sapi
22	1729	98.0	473	2 BAC05013	Bac05013 homo sapi
23	1729	98.0	474	2 BAC85401	Bac85401 homo sapi
24	1729	98.0	474	2 BAC05012	Bac05012 homo sapi
25	1729	98.0	475	2 Q6GMW7	Q6gmW7 homo sapien
26	1729	98.0	475	2 AAH26038	Aah26038 homo sapi
27	1729	98.0	476	2 Q6GMX1	Q6gmX1 homo sapien
28	1729	98.0	476	2 BAC05017	Bac05017 homo sapi
29	1729	98.0	477	2 BAC85394	Bac85394 homo sapi
30	1729	98.0	477	2 BAC85697	Bac85697 homo sapi
31	1729	98.0	477	2 BAC05018	Bac05018 homo sapi

## ALIGNMENTS

### RESULT 1

ID	GCI_HUMAN	STANDARD	PRT	330 AA
AC	P01857			
DT	21-JUL-1986 (Rel. 01, Created)			
DT	21-JUL-1986 (Rel. 01, Last sequence update)			
DT	01-OCT-2004 (Rel. 45, Last annotation update)			
DE	IG gamma-1 chain C region.			
GN	Name=IGHG1;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=82274238; PubMed=6287432;			
RA	Ellison J.W., Berson B.J., Hood L.E.;			
RT	"The nucleotide sequence of a human immunoglobulin C gamma gene."			
RL	Nucleic Acids Res. 10:4071-4079(1982).			
RN	[2]			
RP	SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).			
RX	MEDLINE=71064024; PubMed=5489771;			
RA	Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,			
RA	Waxdal M.J., Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. VII. Amino acid sequence of heavy-chain cyanogen bromide fragments H1-H4."			
RL	Biochemistry 9:3161-3170(1970).			
RN	[3]			
RP	SEQUENCE OF 136-329 (EU).			
RX	MEDLINE=71064025; PubMed=5530842;			
RA	Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,			
RA	Edelman G.M.;			
RT	"The covalent structure of a human gamma G-immunoglobulin. 8. Amino acid sequence of heavy-chain cyanogen bromide fragments H5-H7."			
RL	Biochemistry 9:3171-3181(1970).			
RN	[4]			
RP	SEQUENCE (MYELOMA PROTEIN NIE).			
RX	MEDLINE=77070269; PubMed=826475;			
RA	Ponstingl H., Hilschmann N.;			
RT	"The rule of antibody structure. The primary structure of a monoclonal IgG1 immunoglobulin (myeloma protein Nie). III. The chymotryptic peptides of the H-chain, alignment of the tryptic peptides and discussion of the complete structure."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).			
RN	[5]			
RP	SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.			
RX	MEDLINE=83289131; PubMed=684994;			
RA	Schmidt W.E., Jung W.-D., Palm W., Hilschmann N.;			
RT	"Three-dimensional structure determination of antibodies. Primary structure of crystallized monoclonal immunoglobulin IgG1 KOL, I."			
RL	Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).			
RN	[6]			
RP	DISULFIDE BONDS.			
RX	MEDLINE=71064027; PubMed=4923144;			

Bac85174 homo sapi  
Bac85436 homo sapi  
Bac86514 homo sapi  
Aah06402 homo sapi  
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Bac85350 homo sapi  
Q6in78 homo sapien  
Q6n089 homo sapien  
Cae45781 homo sapi  
Aah37361 homo sapi  
Bac85172 homo sapi  
Bac05014 homo sapi  
Q6p055 homo sapien  
Aah65820 homo sapi

32 1729 98.0 478 2 BAC85174  
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37 1729 98.0 474 2 BAC85350  
38 1726 97.8 466 2 Q6in78  
39 1726 97.8 472 2 Q6n089  
40 1726 97.8 472 2 Cae45781  
41 1725 97.8 467 2 AAH37361  
42 1725 97.8 470 2 BAC85172  
43 1725 97.8 471 2 BAC05014  
44 1725 97.8 473 2 Q6P055  
45 1725 97.8 473 2 AAH65820

RA Gall W.E., Edelman G.M.;  
RT "The covalent structure of a human gamma G-immunoglobulin. X.  
RL Biochemistry 9:3188-3196(1970).  
RN [7]  
RP DISULFIDE BONDS.  
RX MEDLINE=770267; PubMed=1002129;  
RA Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
RT "Rule of antibody structure. The primary structure of a monoclonal  
RT IgG1 immunoglobulin (myeloma protein Nie), I: purification and  
RT characterization of the protein, the L- and H-chains, the cyanogen  
RT bromide cleavage products, and the disulfide bridges.";  
RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
RN [8]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
RX MEDLINE=81208100; PubMed=7236608;  
RA Deisenhofer J.;  
RT "Crystallographic refinement and atomic models of a human Fc fragment  
RT and its complex with fragment B of protein A from Staphylococcus  
RT aureus at 2.9- and 2.8-A resolution.";  
RL Biochemistry 20:2361-2370(1981).  
CC GIM(1) markers: Nie has the GIM(17) allotypic marker, 97-K, and the  
CC GIM(3) marker and the GIM (non-1) markers.  
CC -!- MISCELLANEOUS: Nie also differs in the amidation states of 35,  
CC 115, 198, 269 and 272.  
CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues  
CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
CC 268-272.  
CC -!- MISCELLANEOUS: KOL also differs in the amidation states of  
CC residues 198, 267 and 272.  
CC -----  
CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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CC -----  
DR EMBL: J00228; AAC82527.1; ALT\_INIT.  
DR PIR: A93433; GHHD.  
DR PDB: 1AJ7; X-ray; H=1-103.  
DR PDB: 1D5B; X-ray; B/H=1-101.  
DR PDB: 1D5I; X-ray; H=1-101.  
DR PDB: 1D6V; X-ray; H=1-101.  
DR PDB: 1DN2; X-ray; A/B=120-326.  
DR PDB: 1E4K; X-ray; A/B=106-329.  
DR PDB: 1FC1; X-ray; A/B=106-329.  
DR PDB: 1FC2; X-ray; D=106-329.  
DR PDB: 1FCC; X-ray; A=121-326.  
DR PDB: 1H2H; X-ray; H/K=1-330.  
DR PDB: 1I7Z; X-ray; B/D=1-103.  
DR PDB: 1IIS; X-ray; A/B=107-330.  
DR PDB: 1LIX; X-ray; A/B=107-330.  
DR PDB: 1L6X; X-ray; A=120-326.  
DR PDB: 1OQX; X-ray; A/B=119-330.  
DR PDB: 2RCS; X-ray; H=1-103.  
DR Genew; HGNC:5525; IGHG1.  
DR MIM: 147100; ..  
DR GO: GO:0005624; C:membrane fraction; NAS.  
DR GO: GO:0003823; F:antigen binding; TAS.  
DR GO: GO:0006955; P:immune response; NAS.  
DR InterPro; IPR007110; Ig-like.  
DR InterPro; IPR003006; Ig\_MHC.  
DR Pfam; PF00047; Ig; 3.  
DR PROSITE; PS00835; IG LIKE; 3.  
DR PROSITE; PS00290; IG\_VHC; 2.  
KW 3D-structure; Direct\_protein sequencing; Glycoprotein;  
KW Immunoglobulin C region; Immunoglobulin domain.  
FT NON\_TER 1 1  
FT DOMAIN 1 98 CH1.  
FT Hinge. 99 110

FT DOMAIN 111 223  
FT DOMAIN 224 330  
FT DISULFID 27 83  
FT DISULFID 103 103 Interchain (with light chain).  
FT DISULFID 109 109 Interchain (with heavy chain).  
FT DISULFID 112 112 Interchain (with heavy chain).  
FT DISULFID 144 204  
FT DISULFID 250 308  
FT CARBOHYD 180 180  
FT VARIANT 97 97  
FT N-linked (GlcNAc...)  
FT K -> R (in G1M(3) marker).  
FT /FTID=VAR\_003896.  
FT D -> E (in G1M(non-1) marker).  
FT /FTID=VAR\_003897.  
FT L -> M (in G1M(non-1) marker).  
FT /FTID=VAR\_003898.  
FT VARIANT 239 239  
FT VARIANT 241 241  
FT STRAND 23 24  
FT STRAND 26 33  
FT STRAND 38 38  
FT STRAND 41 41  
FT TURN 42 45  
FT TURN 48 49  
FT STRAND 50 52  
FT STRAND 57 58  
FT TURN 59 61  
FT STRAND 62 71  
FT HELIX 73 75  
FT TURN 76 78  
FT STRAND 82 87  
FT TURN 88 91  
FT STRAND 92 97  
FT TURN 102 103  
FT STRAND 122 126  
FT HELIX 130 134  
FT TURN 136 137  
FT STRAND 141 149  
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FT TURN 163 164  
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FT TURN 179 180  
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FT TURN 198 199  
FT STRAND 202 207  
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FT STRAND 215 219  
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FT STRAND 238 242  
FT HELIX 245 256  
FT STRAND 261 266  
FT TURN 267 268  
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FT STRAND 274 276  
FT STRAND 280 281  
FT TURN 283 284  
FT STRAND 287 296  
FT TURN 297 301  
FT HELIX 302 303  
FT TURN 306 311  
FT STRAND 313 314  
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Best Local Similarity 97.9%; Pred No. 1e-117;  
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DB 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVNSGALTSGVHTFPAVLQSS 60





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121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
257 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 316
181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
317 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 376
241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGVFFLYSKLTVDKSRW 300
377 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGVFFLYSKLTVDKSRW 436
301 QGQNVFSCSVNHEALHNHYQOQSLSLSPGK 330
437 QGQNVFSCSVNHEALHNHYQOQSLSLSPGK 466

RESULT 6
BAC85173 PRELIMINARY; PRT; 467 AA.
AC BAC85173;
DT 02-MAR-2004 (TremBLrel. 27, Created)
DT 02-MAR-2004 (TremBLrel. 27, Last sequence update)
CDNA FLJ26001 fis, clone DMC07585, highly similar to Ig gamma-1 chain
C region.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dermoid tumor;
RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RA "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK129512; BAC85173.1; -.
SQ SEQUENCE 467 AA; 50782 MW; 632AEA2D6CD248F5 CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 467;
Best Local Similarity 97.9%; Pred. No. 1.6e-117;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 60
138 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 197
61 GLYSLSVVTVFPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPELGG 120
198 GLYSLSVVTVFPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPELGG 257
121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
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181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
318 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 377
241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGVFFLYSKLTVDKSRW 300
378 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGVFFLYSKLTVDKSRW 437
301 QGQNVFSCSVNHEALHNHYQOQSLSLSPGK 330
438 QGQNVFSCSVNHEALHNHYQOQSLSLSPGK 467
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RESULT 7

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BAC85175 PRELIMINARY; PRT; 468 AA.
ID BAC85175;
AC BAC85175;
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DT 02-MAR-2004 (TremBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TremBLrel. 27, Last annotation update)
DE CDNA FLJ26006 fis, clone DMC08725, highly similar to Ig gamma-1 chain
C region.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dermoid tumor;
RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RA "NEDO human cDNA sequencing project.";
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK129517; BAC85175.1; -.
SQ SEQUENCE 468 AA; 51266 MW; 11C519D86AE3D44B CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 468;
Best Local Similarity 97.9%; Pred. No. 1.6e-117;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 60
139 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNVNSGALTSGVHTFPAVLQSS 198
61 GLYSLSVVTVFPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPELGG 120
199 GLYSLSVVTVFPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHCTCPCPAPELGG 258
121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180
259 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 318
181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240
319 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 378
241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGVFFLYSKLTVDKSRW 300
379 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGVFFLYSKLTVDKSRW 438
301 QGQNVFSCSVNHEALHNHYQOQSLSLSPGK 330
439 QGQNVFSCSVNHEALHNHYQOQSLSLSPGK 468

RESULT 8
BAC85444 PRELIMINARY; PRT; 468 AA.
ID BAC85444;
AC BAC85444;
DT 02-MAR-2004 (TremBLrel. 27, Created)
DT 02-MAR-2004 (TremBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TremBLrel. 27, Last annotation update)
DE CDNA FLJ27334 fis, clone FMS09201, highly similar to Ig gamma-1 chain
C region.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
RA Sugano S.;
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RT "NEDO human cDNA sequencing project.;"
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK130844; BAC95444.1; -
SQ SEQUENCE 468 AA; 51224 MW; 9280ACAD6817FC20 CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 468;
Best Local Similarity 97.9%; Pred. No. 1.6e-117; Indels 0; Gaps 0;
Matches 323; Conservative 3; Mismatches 4;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 60
Db 139 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 198
QY 61 GLYSLSVVTVPSSSLGTQYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGG 120
Db 199 GLYSLSVVTVPSSSLGTQYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGG 258
QY 121 PSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 259 PSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 318
QY 181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 319 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 378
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 300
Db 379 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 438
QY 301 QQGVNFSCSVWHEALHNNHYQQRSLSPGK 330
Db 439 QQGVNFSCSVWHEALHNNHYQQRSLSPGK 468

RESULT 9
Q7Z7P5 PRELIMINARY; PRT; 469 AA.
AC Q7Z7P5;
AD Q7Z7P5;
DT 01-OCT-2003 (TrEMBLrel. 25, Created)
DT 01-OCT-2003 (TrEMBLrel. 25, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE IGHG1 protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.;"
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;

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RA Strausberg R.;
RL Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC051328; AAH51328.1; -
DR InterPro; IPR007110; IG-like.
DR InterPro; IPR003597; IG_c1.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PF07654; C1-set; 3.
DR Pfam; PF00047; IG; 1.
DR SMART; SM00406; IGV; 1.
DR PROSITE; PS00835; IG_LIKE; 4.
DR PROSITE; PS00290; IG_MHC; UNKNOWN 2.
SQ SEQUENCE 469 AA; 51395 MW; C8D5BBL2BAAF795C CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 469;
Best Local Similarity 97.9%; Pred. No. 1.6e-117;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 60
Db 140 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSNWNSGALTSGVHTFPAVLQSS 199
QY 61 GLYSLSVVTVPSSSLGTQYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGG 120
Db 200 GLYSLSVVTVPSSSLGTQYICNVNHKPSNTKVDKVEPKSCDKHTHTCPCPAPELIGG 259
QY 121 PSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
Db 260 PSVLEFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 319
QY 181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 320 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 379
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 300
Db 380 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 439
QY 301 QQGVNFSCSVWHEALHNNHYQQRSLSPGK 330
Db 440 QQGVNFSCSVWHEALHNNHYQQRSLSPGK 469

RESULT 10
Q6PJA4 PRELIMINARY; PRT; 470 AA.
AC Q6PJA4;
AD Q6PJA4;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
[1]
RN SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Villalón D.K., Muzny K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson G.G.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smalhus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.;"
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
[2]
RN SEQUENCE FROM N.A.
RC TISSUE=Spleen;

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Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences".  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]  
SEQUENCE FROM N.A.  
TISSUE=Primary B-Cells;  
Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
EMBL: BC018747; AAH18747.1; -  
InterPro: IPR003599; IG-like.  
InterPro: IPR007110; IG-like.  
InterPro: IPR003597; IG ci.  
InterPro: IPR003006; IG\_MHC.  
InterPro: IPR003596; IG v.  
Pfam: PF07654; CI-set; 3.  
Pfam: PF00047; IG; 4.  
SMART: SM00409; IG; 2.  
SMART: SM00407; IG ci; 3.  
SMART: SM00406; IGV; 1.  
PROSITE: PS00835; IG LIKE; 4.  
PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
Hypothetical protein.  
SEQUENCE 470 AA; 51715 MW; 7849556a11PD7D99 CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 470;  
Best Local Similarity 97.9%; Pred. No. 1.6e-117;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTKGPSVFPLAPSSKSTSGGTAALGLVQDYPPFVTVSWNSGALTSGVHTFPAVLQSS 60  
141 ASTKGPSVFPLAPSSKSTSGGTAALGLVQDYPPFVTVSWNSGALTSGVHTFPAVLQSS 200  
61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKHTTCPCPAPPELLGG 120  
201 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKHTTCPCPAPPELLGG 260  
121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNKTKPREEQYN 180  
261 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNKTKPREEQYN 320  
181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 240  
321 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 380  
241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300  
381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 440  
301 QQGNVFCSCVMHEALHNHYQKRSLSLSPGK 330  
441 QQGNVFCSCVMHEALHNHYQKRSLSLSPGK 470

RESULT 11  
7Z5W1 PRELIMINARY; PRT; 470 AA.  
Q7Z5W1  
01-OCT-2003 (Tremblrel. 25, Created)  
01-OCT-2003 (Tremblrel. 25, Last sequence update)  
01-WAR-2004 (Tremblrel. 26, Last annotation update)  
Hypothetical protein.  
Homo sapiens (Human).  
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
TISSUE=Spleen;  
MEDLINE=22388257; PubMed=12477932;  
Straussberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Ioquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton E., Kettingman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.M., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S., Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E., Jones S.J., Marra M.A.;  
"Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences".  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).

[2]  
SEQUENCE FROM N.A.  
TISSUE=Spleen;  
Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
EMBL: BC053984; AAH53984.1; -  
InterPro: IPR007110; IG-like.  
InterPro: IPR003597; IG ci.  
InterPro: IPR003006; IG\_MHC.  
InterPro: IPR003596; IG v.  
Pfam: PF07654; CI-set; 3.  
Pfam: PF00047; IG; 1.  
DR SMART: SM00406; IGV; 1.  
DR PROSITE: PS00835; IG LIKE; 4.  
DR PROSITE: PS00290; IG\_MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;

Query Match 98.0%; Score 1729; DB 2; Length 470;  
Best Local Similarity 97.9%; Pred. No. 1.6e-117;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTKGPSVFPLAPSSKSTSGGTAALGLVQDYPPFVTVSWNSGALTSGVHTFPAVLQSS 60  
141 ASTKGPSVFPLAPSSKSTSGGTAALGLVQDYPPFVTVSWNSGALTSGVHTFPAVLQSS 200  
61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKHTTCPCPAPPELLGG 120  
201 GLYSLSSVTVTPSSSLGTQTYICNVNHPKSNKTKVDKVPKSCDKHTTCPCPAPPELLGG 260  
121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNKTKPREEQYN 180  
261 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNKTKPREEQYN 320  
181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 240  
321 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 380  
241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300  
381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 440  
301 QQGNVFCSCVMHEALHNHYQKRSLSLSPGK 330  
441 QQGNVFCSCVMHEALHNHYQKRSLSLSPGK 470

RESULT 12  
BAC85235 PRELIMINARY; PRT; 470 AA.  
ID BAC85235  
AC BAC85235;  
DT 02-MAR-2004 (Tremblrel. 27, Created)  
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)  
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)

DE CDNA FLJ26276 fis, clone DMC06522, highly similar to Ig gamma-1 chain  
 DE C region.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.  
 RN NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Dermoid tumor;  
 RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,  
 RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,  
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,  
 RA Kawakami B., Nagai K., Isogai T., Sugano S.;  
 RT "NEDO human cDNA sequencing project";  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK129787; BAC85235.1; -;  
 SQ SEQUENCE 470 AA; 51090 MW; 460F4717D4528A16 CRC64;  
 Query Match 98.0%; Score 1729; DB 2; Length 470;  
 Best Local Similarity 97.9%; Pred. No. 1.6e-117;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPPPTVSWNSGALTSGVHTFPAVLQSS 60  
 Db 141 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPPPTVSWNSGALTSGVHTFPAVLQSS 200  
 Qy 61 GLYSLSSVVTVPSSSLGTQYICNVNHPKSTNTKDKKVEPKSCDKTHCTCPCPAPPELLGG 120  
 Db 201 GLYSLSSVVTVPSSSLGTQYICNVNHPKSTNTKDKKVEPKSCDKTHCTCPCPAPPELLGG 260  
 Qy 121 PSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEHNHVKTKPREEQYN 180  
 Db 261 PSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEHNHVKTKPREEQYN 320  
 Qy 181 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 Db 321 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 380  
 Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW 300  
 Db 381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW 440  
 Qy 301 QQGNVFCSWMEALHNHYQOQSLSLSPGK 330  
 Db 441 QQGNVFCSWMEALHNHYQOQSLSLSPGK 470  
 RESULT 14  
 AAH62336 PRELIMINARY; PRT; 470 AA.  
 ID AAH62336  
 AC AAH62336  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC062336; AAH62336.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 470 AA; 51524 MW; CC861ACD6B7C1CC6 CRC64;

DE CDNA FLJ26276 fis, clone DMC06522, highly similar to Ig gamma-1 chain  
 DE C region.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.  
 RN NCBI\_TaxID=9606;  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Dermoid tumor;  
 RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,  
 RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,  
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,  
 RA Kawakami B., Nagai K., Isogai T., Sugano S.;  
 RT "NEDO human cDNA sequencing project";  
 RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; AK129787; BAC85235.1; -;  
 SQ SEQUENCE 470 AA; 51090 MW; 460F4717D4528A16 CRC64;  
 Query Match 98.0%; Score 1729; DB 2; Length 470;  
 Best Local Similarity 97.9%; Pred. No. 1.6e-117;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 Qy 1 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPPPTVSWNSGALTSGVHTFPAVLQSS 60  
 Db 141 ASTKGPSVFLAPSSKSTSGGTAALGCLVKDYFPPPTVSWNSGALTSGVHTFPAVLQSS 200  
 Qy 61 GLYSLSSVVTVPSSSLGTQYICNVNHPKSTNTKDKKVEPKSCDKTHCTCPCPAPPELLGG 120  
 Db 201 GLYSLSSVVTVPSSSLGTQYICNVNHPKSTNTKDKKVEPKSCDKTHCTCPCPAPPELLGG 260  
 Qy 121 PSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEHNHVKTKPREEQYN 180  
 Db 261 PSVFLFPKPKDLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEHNHVKTKPREEQYN 320  
 Qy 181 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 Db 321 STYRVSVLTVLHQNMMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 380  
 Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW 300  
 Db 381 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTPVLDSDGSFFLYSKLTVDKSRW 440  
 Qy 301 QQGNVFCSWMEALHNHYQOQSLSLSPGK 330  
 Db 441 QQGNVFCSWMEALHNHYQOQSLSLSPGK 470  
 RESULT 14  
 AAH62336 PRELIMINARY; PRT; 470 AA.  
 ID AAH62336  
 AC AAH62336  
 DT 02-MAR-2004 (TrEMBLrel. 27, Created)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.D., Feingold E.A., Grouse L.H., Derge J.G.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haie F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Faney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RT "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Spleen;  
 RA Strausberg R.;  
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC062336; AAH62336.1; -;  
 KW Hypothetical protein.  
 SQ SEQUENCE 470 AA; 51524 MW; CC861ACD6B7C1CC6 CRC64;



Query Match 98.0%; Score 1729; DB 2; Length 470;  
Best Local Similarity 97.9%; Pred. No. 1.6e-117;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYPPETVTVSWNSGALTSVGHFFPAVLQSS 60  
141 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYPPETVTVSWNSGALTSVGHFFPAVLQSS 200  
61 GLYSLSSVTVVPSSSSLGTQYIICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120  
201 GLYSLSSVTVVPSSSSLGTQYIICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 260  
121 PSVFLFPKPKDITLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
261 PSVFLFPKPKDITLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 320  
181 STYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 240  
321 STYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 380  
241 LTKNOVSLTCLVKGFPYSDIAVESNGQPNNTKTPPVLDSDGSGFFLYSKLTVDKSRW 300  
381 LTKNOVSLTCLVKGFPYSDIAVESNGQPNNTKTPPVLDSDGSGFFLYSKLTVDKSRW 440  
301 QQGNVFCVSMHEALHNHYQOQSLSLSPGK 330  
441 QQGNVFCVSMHEALHNHYQOQSLSLSPGK 470

SU15  
H14258  
AAH14258 PRELIMINARY; PRT; 470 AA.  
AAH14258;  
02-MAR-2004 (TrEMBLrel. 27, Created)  
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)  
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)  
Hypothetical protein.  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
NCBI\_TaxID=9606;  
[1]  
SEQUENCE FROM N.A.  
TISSUE=Primary B-Cells;  
MEDLINE=22388257; PubMed=12477932;  
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
Klausner R.D., Collins P.S., Wagner L., Shenmen C.M., Schuler G.D.,  
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
Villalón D.K., Murny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
Krzyszewski M.I., Skalska U., Smalios D.E., Schnerch A., Schein J.E.,  
Jones S.J., Marra M.A.;  
[2]  
Generation and initial analysis of more than 15,000 full-length human  
and mouse cDNA sequences.;  
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
[2]  
SEQUENCE FROM N.A.  
TISSUE=Primary B-Cells;  
Strausberg R.;  
Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.  
EMBL; BC014258; AAH14258.1; -;  
Hypothetical protein.

SQ SEQUENCE 470 AA; 51514 MW; BFD56EP8157DBA79 CRC64;  
Query Match 98.0%; Score 1729; DB 2; Length 470;  
Best Local Similarity 97.9%; Pred. No. 1.6e-117;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYPPETVTVSWNSGALTSVGHFFPAVLQSS 60  
141 ASTKGPSVFFPLAPSSKSTSGTAAALGCLVKDYPPETVTVSWNSGALTSVGHFFPAVLQSS 200  
61 GLYSLSSVTVVPSSSSLGTQYIICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120  
201 GLYSLSSVTVVPSSSSLGTQYIICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 260  
121 PSVFLFPKPKDITLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
261 PSVFLFPKPKDITLIMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 320  
181 STYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 240  
321 STYRVSVLTVLHQDMLNGKEYCKVSNKALPAPIETISKAKVQPREPOVYTLPPSRDE 380  
241 LTKNOVSLTCLVKGFPYSDIAVESNGQPNNTKTPPVLDSDGSGFFLYSKLTVDKSRW 300  
381 LTKNOVSLTCLVKGFPYSDIAVESNGQPNNTKTPPVLDSDGSGFFLYSKLTVDKSRW 440  
301 QQGNVFCVSMHEALHNHYQOQSLSLSPGK 330  
441 QQGNVFCVSMHEALHNHYQOQSLSLSPGK 470

Search completed: October 27, 2004, 17:03:55  
Job time : 151.733 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

protein - protein search, using sw model

on: October 27, 2004, 16:31:18 ; Search time 126.246 seconds  
(without alignments)  
937.702 Million cell updates/sec

US-10-000-439-2

fect score: 1764

quence: 1 ASTKGPSVFLAPSSKSTG.....MHEALHHYQQRSLSLSPGK 330

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Gapop 10.0 , Gapext 0.5

arched: 2002273 seqs, 358729299 residues

tal number of hits satisfying chosen parameters: 2002273

imum DB seq length: 0  
imum DB seq length: 2000000000

st-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

atabase : A\_Geneseq\_23Sep04:\*

- 1: Geneseq1980s:\*
- 2: Geneseq1990s:\*
- 3: Geneseq2000s:\*
- 4: Geneseq2001s:\*
- 5: Geneseq2002s:\*
- 6: Geneseq2003as:\*
- 7: Geneseq2003bs:\*
- 8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1764	100.0	330	6	AAO19664 Human IGG
2	1729	98.0	330	4	ABO4071 Zcytor 10
3	1729	98.0	330	5	AAW47856 Human Ig-
4	1729	98.0	330	5	AAE21960 Human dea
5	1729	98.0	330	5	ABB81641 Human IGG
6	1729	98.0	330	5	ABB05736 Human imm
7	1729	98.0	330	6	ABP71856 Human IGG
8	1729	98.0	330	6	AAE32915 Human imm
9	1729	98.0	330	6	AAE32627 Human imm
10	1729	98.0	330	6	ABR82103 Human DR6
11	1729	98.0	330	6	AAO31102 Human A2-
12	1729	98.0	330	6	ABR55836 Anti-Ang-
13	1729	98.0	330	6	AAO30893 Human imm
14	1729	98.0	330	7	ADF11389 Anti-OpGL
15	1729	98.0	330	7	ADG97351 Human IGG
16	1729	98.0	330	7	ADF83605 Cycokine
17	1729	98.0	330	7	ADF75001 Human Ig
18	1729	98.0	330	8	ADM41537 Anti-Inte
19	1729	98.0	330	8	ADM68911 Human IGG
20	1729	98.0	332	8	ADL35095 Human IGG
21	1729	98.0	333	8	ADJ95912 Human IGG
22	1729	98.0	333	8	ADL2761 Human ant
23	1729	98.0	351	2	AAK43685 Human kap
24	1729	98.0	356	8	ADJ95976 Immunoglo
25	1729	98.0	371	1	AAp91918 Sequence

26	1729	98.0	442	6	ABR39465 Humanised
27	1729	98.0	442	6	ABR39474 Humanised
28	1729	98.0	442	6	ABU08311 Humanised
29	1729	98.0	442	6	ABU08320 Humanised
30	1729	98.0	442	6	ABR39793 Humanised
31	1729	98.0	442	6	ABB80113 Deglycosy
32	1729	98.0	442	6	ABB80109 Heavy Cha
33	1729	98.0	442	7	ABE94066 Humanised
34	1729	98.0	442	7	ADG94075 Humanised
35	1729	98.0	442	8	ADN61714 Humanised
36	1729	98.0	444	6	AAE35327 Humanised
37	1729	98.0	444	6	AAE34876 BIWA/8 a
38	1729	98.0	444	8	ADL15443 Humanised
39	1729	98.0	444	8	ADO00851 Humanised
40	1729	98.0	445	6	AAO31101 Human A2-
41	1729	98.0	445	7	ADF11421 2E11 anti
42	1729	98.0	445	7	ADF11429 18B2 anti
43	1729	98.0	446	7	ADF11435 2D8 anti-
44	1729	98.0	446	7	ADF11437 9H7 anti-
45	1729	98.0	446	7	ADF11433 16E1 anti

ALIGNMENTS

RESULT 1  
AAO19664  
ID AAO19664 standard; protein; 330 AA.  
XX  
AC AAO19664;  
XX  
DT 28-MAR-2003 (first entry)  
XX  
DE Human IgG1 heavy chain constant region.  
XX  
KW Human; IgG1; immunoglobulin G; immunotherapy; immune disease;  
KW Pepsilon receptor; autoimmune disease; constant region; heavy chain;  
KW antiasthmatic; antiallergic; antiinflammatory; dermatological;  
KW antiarthritic; antirheumatic; antidiabetic; neuroprotective.  
XX  
OS Homo sapiens.  
XX  
PN WO200288317-A2.  
XX  
PD 07-NOV-2002.  
XX  
PF 01-MAY-2002; 2002WO-US013527.  
XX  
PR 01-MAY-2001; 2001US-00847208.  
XX  
PA 24-OCT-2001; 2001US-00000439.  
XX  
(REGC ) UNIV CALIFORNIA.  
XX  
PI Saxon A, Zhang K, Zhu D;  
XX  
DR WPI; 2003-103456/09.  
XX  
PT New fusion molecules comprising polypeptide sequences that bind to IgG  
PT inhibitory receptor and native IgE receptor, useful for treating IgE-  
PT mediated hypersensitivity reactions, e.g. asthma or allergies, or  
XX autoimmune diseases.  
XX  
PS Claim 64; Fig 2; 116pp; English.  
XX  
CC The present invention relates to a fusion molecule comprising a first  
CC polypeptide sequence capable of specific binding to a native IgG  
CC inhibitory receptor consisting of an immune receptor tyrosine-based  
CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
CC functionally connected to a second polypeptide sequence capable of  
CC specific binding directly or indirectly to a native IgE receptor  
CC (FcpsilonE). Also provided are nucleotide sequences encoding such a  
CC fusion protein. The fusion molecules and compositions are useful for  
CC treating an IgE-mediated biological response, preferably an IgE-mediated



Homo sapiens.  
WO200183529-A2.  
08-NOV-2001.  
28-APR-2001; 2001WO-US013932.  
28-APR-2000; 2000US-0200298P.  
(PLAN-) PLANET BIOTECHNOLOGY INC.  
Larrick JW, Wycoff KL;  
WPI; 2002-041481/05.  
N-PSDB; ABA05265.  
Immunoadhesin for treating human rhinovirus infection comprises chimeric intercellular adhesion molecule-1, and optionally a J chain and secretory component in association.  
Disclosure; Fig 7; 138pp; English.  
The invention relates to an immunoadhesin comprising: (a) a chimeric intercellular adhesion molecule (ICAM)-1 comprising a rhinovirus receptor protein linked to at least a portion of an immunoglobulin heavy chain; and (b) optionally a J chain and secretory component associated with the chimeric ICAM-1 molecule. The immunoadhesin has plant-specific glycosylation and virucide activity. The immunoadhesin is useful for reducing infection by human rhinovirus (HRV) and hence the initiation or spread of the common cold by HRV. The immunoadhesin binds to HRV and reduces its infectivity, competing with cell surface ICAM-1 for binding sites, interfering with virus entry or uncoating and directing premature release of viral RNA and formation of empty capsids. Expression of the immunoadhesin in plants would be tetrameric, rather than dimeric. Immunoadhesin having multiple binding sites have a higher effective affinity for the virus, thereby increasing the effectiveness of the immunoadhesin. Association of secretory component and immunoglobulin J chain increases the stability of the immunoadhesin in the mucosal environment. Production is significantly less expensive in plants than in animal cell culture and production in plants is safer for human use, since plants are not known to harbor any animal viruses. The present sequence is that of a human immunoglobulin protein sequence, useful to the invention  
Sequence 330 AA;  
Query Match 98.0%; Score 1729; DB 5; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.7e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
61 GLYSLSVVTVPPSSSLGQTQVVCNNHKNPSNTKYDKVPEKSCDKHTCTCPAPPELLGG 120  
61 GLYSLSVVTVPPSSSLGQTQVVCNNHKNPSNTKYDKVPEKSCDKHTCTCPAPPELLGG 120  
121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPRSEQYN 180  
121 PSVFLFPPKPKDITLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPRSEQYN 180  
181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240  
181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240  
241 LTKNQVSLTCLVKGFYPSDIAVEVESNQPNNTKTPPVLDVSGSFYSLKLTVDKSRW 300  
241 LTKNQVSLTCLVKGFYPSDIAVEVESNQPNNTKTPPVLDVSGSFYSLKLTVDKSRW 300  
301 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 330  
|||||

Db 301 QGQNVFSCSVMEALHNHYTQKSLSLSPGK 330  
RESULT 4  
AAE21960  
ID AAE21960 standard; protein; 330 AA.  
XX  
AC AAE21960;  
XX  
DT 25-JUL-2002 (first entry)  
XX  
DE Human death domain containing receptor (DR6) protein-related protein.  
XX  
KW Human; therapy; death domain containing receptor; DR6; receptor; anaemia;  
KW apoptosis; rheumatoid arthritis; eczema; asthma; psoriasis; pancreatitis;  
KW diabetes; cancer; multiple sclerosis; Graves disease; glomerulonephritis;  
KW transplant rejection; systemic lupus erythematosus; hepatitis; cirrhosis;  
KW autoimmune; gastritis; dermatosis; cardiomyopathy; infertility; haemostatic;  
KW H. pylori-associated ulceration; antiinflammatory; vasotropic; virucide;  
KW acquired immunodeficiency syndrome; AIDS; human immunodeficiency virus;  
KW HIV; haemolytic uraemic syndrome; HUS; immunodeficiency; neuroprotective;  
KW adult respiratory distress syndrome; ARDS; cytostatic; thyromimetic;  
KW dermatological; hepatotropic; antibacterial.  
XX  
OS Homo sapiens.  
XX  
FN WO2001:85209-A2.  
XX  
PD 15-NOV-2001.  
XX  
PF 30-APR-2001; 2001WO-US011735.  
XX  
PR 10-MAY-2000; 2000US-0203015P.  
XX  
PA (ELIL) LILLY & CO ELI.  
XX  
PI Heuer JG, Liu J, Na S, Song HY, Yang D;  
XX  
DR WPI; 2002-351283/38.  
XX  
PT Treating or preventing T cell or Th2 cell mediated condition e.g.; asthma  
PT or multiple sclerosis in mammal, comprises administering composition  
PT comprising death domain containing receptor, DR6 agonist or antagonist.  
XX  
PS Disclosure; Page 132-133; 133pp; English.  
XX  
CC The invention relates to a method for treating or preventing a T cell  
CC mediated condition or a Th2 cell mediated condition in a mammal. The  
CC method comprising administering to the mammal a pharmaceutical  
CC composition comprising a death domain containing receptor (DR6) agonist  
CC or antagonist. The method is useful for treating or preventing a T cell  
CC mediated condition or a Th2 cell mediated condition in a mammal. A DR6  
CC agonist is useful in the manufacture of a medicament for treating or  
CC preventing at least one symptom associated with aberrant apoptosis, graft  
CC -versus-host disease (GVHD), rheumatoid arthritis, eczema, asthma, atopy,  
CC inflammatory bowel disease, vasculitis, psoriasis, pancreatitis, insulin-  
CC dependent diabetes mellitus, cancer, multiple sclerosis, Hashimoto's  
CC thyroiditis, Graves disease, transplant rejection, systemic lupus  
CC erythematosus, autoimmune dermatosis, autoimmune cardiopathy, autoimmune  
CC infertility, Behcet's disease, autoimmune gastritis, fibrosing lung  
CC disease, organ rejection after transplantation, thrombotic  
CC thrombocytopenic purpura (TTP), chronic anaemia, myelodysplasia, multiple organ  
CC uraemic syndrome (HUS), aplastic anaemia, myelodysplasia, multiple organ  
CC dysfunction syndrome (MDDS), adult respiratory distress syndrome (ARDS)  
CC or a condition or symptom related to the above mentioned diseases in a  
CC mammal. An DR6 antagonist is useful in the manufacture of a medicament  
CC for treating or preventing at least one symptom associated with  
CC immunodeficiency, aberrant apoptosis, bacterial, viral or microbial  
CC infection, complications of infection, human immunodeficiency virus  
CC (HIV), HIV-induced lymphoma, HIV-induced acquired immunodeficiency  
CC syndrome (AIDS), fulminant viral hepatitis B, fulminant viral hepatitis  
CC C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis, H. pylori  
CC associated ulceration, cytoprotection during cancer treatment.

CC recuperation from chemotherapy, recuperation from irradiation therapy, or  
 CC a condition or symptom related to the above mentioned diseases in a  
 CC mammal. The present sequence is human DR6 protein-related protein  
 XX  
 SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 1.7e-122;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKNTKVDKVPKSCDKTHTCCPCPAPELLGG 120  
 DB 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKNTKVDKVPKSCDKTHTCCPCPAPELLGG 120  
 QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPREQYN 180  
 DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPREQYN 180  
 QY 181 STYRVSVLTVLHQWMNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
 DB 181 STYRVSVLTVLHQWMNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFYFLYSLKLTVDKGRW 300  
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFYFLYSLKLTVDKGRW 300  
 QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330  
 DB 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 5  
 ID ABB81641 standard; protein; 330 AA.  
 AC ABB81641;  
 XX  
 XX 25-SEP-2002 (first entry)  
 DE Human IgG gamma 1 heavy chain SEQ ID NO:15.  
 KW Human; zcytor19; cytokine receptor; immunosuppressive; cytostatic;  
 KW antirheumatic; antiarthritic; neuroprotective; antiinflammatory;  
 KW antidiabetic; nephrotropic; dermatological; anti-HIV; haemostatic;  
 KW vaccine; immune system; T-cell specific leukaemia; lymphoma; lupus;  
 KW autoimmune disease; rheumatoid arthritis; multiple sclerosis; HIV;  
 KW diabetes mellitus; inflammatory bowel disease; Crohn's disease; asthma;  
 KW immunologic renal disease; glomerulonephritis; vasculitis; polyarteritis;  
 KW mesangioproliferative disease; chronic lymphocytic leukaemia; bronchitis;  
 KW secondary glomerulonephritis; scleroderma; amyloidosis; multiple myeloma;  
 KW haemolytic uraemic syndrome; renal neoplasm; urological neoplasm;  
 KW emphysema; chronic airway disease.  
 XX  
 OS Homo sapiens.  
 XX  
 XX WO20024209-A2.  
 XX  
 XX 06-JUN-2002.  
 XX  
 XX 28-NOV-2001; 2001WO-US044808.  
 XX  
 XX 28-NOV-2000; 2000US-0253561P.  
 XX  
 XX 07-FEB-2001; 2001US-0267211P.  
 XX  
 XX (ZYMO) ZYMOGENETICS INC.  
 XX  
 XX Presnell SR, Xu W, Novak JB, Whitmore TE, Grant FU;  
 FI  
 XX WPI; 2002-527700/56.  
 XX  
 XX

DR N-PSDB; ABQ73076.  
 XX Novel Zcytor19 polypeptides and polynucleotides useful for stimulating  
 PT immune responses in animals for producing antibodies, and for treating  
 PT autoimmune diseases, leukemia and asthma.  
 XX  
 PS Example 7; Page 171-172; 200pp; English.  
 XX  
 CC The present invention describes an isolated human zcytor19 protein (I),  
 CC and truncated zcytor19 proteins. (I) has immunosuppressive, cytostatic,  
 CC antirheumatic, antiarthritic, neuroprotective, antiinflammatory, cytostatic,  
 CC antidiabetic, nephrotropic, dermatological, anti-HIV and haemostatic  
 CC activities, and can be used in vaccines. (I) or an antibody binding (I)  
 CC can be used for suppressing the immune system for reducing rejection of  
 CC tissue or organ transplants and grafts and for treating T-cell specific  
 CC leukaemias or lymphomas and autoimmune diseases including rheumatoid  
 CC arthritis, multiple sclerosis, diabetes mellitus, inflammatory bowel  
 CC disease and Crohn's disease. The antibodies can also be used for treating  
 CC immunologic renal diseases, glomerulonephritis, mesangioproliferative  
 CC disease, chronic lymphocytic leukaemia, secondary glomerulonephritis or  
 CC vasculitis associated with lupus, polyarteritis, scleroderma, HIV-related  
 CC diseases, amyloidosis and haemolytic uraemic syndrome. (I) and the  
 CC antibodies can also be used for renal or urological neoplasms and  
 CC multiple myelomas, asthma, bronchitis, emphysema and other chronic airway  
 CC diseases. Human zcytor19 is located to chromosome 1, more specifically to  
 CC chromosome 1p36.11. The present sequence represents a human IgG gamma 1  
 CC heavy chain protein, which is used in an example from the present  
 CC invention  
 XX  
 SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 1.7e-122;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 DB 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 QY 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKNTKVDKVPKSCDKTHTCCPCPAPELLGG 120  
 DB 61 GLYSLSVVTVFPSSSLGTQTYICNVNHPKNTKVDKVPKSCDKTHTCCPCPAPELLGG 120  
 QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPREQYN 180  
 DB 121 PSVFLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVVHNVTKPREQYN 180  
 QY 181 STYRVSVLTVLHQWMNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
 DB 181 STYRVSVLTVLHQWMNGKEYCKVSNKALPAPIEKTISKAKGQPREPQVYTLPPSRDE 240  
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFYFLYSLKLTVDKSRW 300  
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFYFLYSLKLTVDKSRW 300  
 QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330  
 DB 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 6  
 ABB05736  
 ID ABB05736 standard; protein; 330 AA.  
 XX  
 AC ABB05736;  
 XX  
 XX 01-MAY-2002 (first entry)  
 XX  
 XX Human immunoglobulin G gamma 1 protein sequence SEQ ID NO:38.  
 XX  
 XX Zcytor17; chromosome 5; Sg11; cytokine receptor; immunomodulatory;  
 KW antirheumatic; antiviral; antirheumatic; antiarthritic; cytostatic;  
 KW muscular; lymphoid; immune; inflammatory; splenic; blood; bone;  
 KW

infection; immunosuppression; cytotoxicity; leukopenia; Crohn's disease; autoimmune disease; rheumatoid arthritis; multiple sclerosis; cancer; inflammatory disease; pancreatitis; inflammatory bowel disease.

Homo sapiens.

WO200200721-A2.

03-JAN-2002.

26-JUN-2001; 2001WO-US020484.

26-JUN-2000; 2000US-0214282P.

29-JUN-2000; 2000US-0214955P.

08-FEB-2001; 2001US-0267963P.

(ZYMO.) ZYMOGENETICS INC.

Sprecher CA, Presnell SR, Gao Z, Whitmore TE, Kuijper JL, Maurer MF;

WPI; 2002-090519/12.

N-PSDB; ABA93797.

Isolated polynucleotide encoding a cytokine receptor zcytor17 which is useful for treating and diagnosing lymphoid, immune, inflammatory, splenic, blood or bone disorders.

Example 17; Page 187-188; 235pp; English.

The present invention describes a cytokine receptor designated zcytor17. Zcytor17 has immunomodulatory, anti-inflammatory, antiviral, cytostatic, antirheumatic, antiarthritic and muscular activities. The zcytor17 proteins are useful for treating and diagnosing lymphoid, immune, inflammatory, splenic, blood or bone disorders. Agonists or anti-zcytor17 antibodies are useful in stimulating cell-mediated immunity and for stimulating lymphocyte proliferation, such as in the treatment of infections involving immunosuppression, including certain viral infections. They are also useful for inducing cytotoxicity and for treating leukopenias. Antagonist of zcytor17 polypeptides are useful for treating autoimmune diseases (e.g. rheumatoid arthritis and multiple sclerosis), inflammatory diseases (e.g. Crohn's disease), cancer, pancreatitis, and inflammatory bowel disease. Zcytor17 was mapped to chromosome 5, specifically to the 5q11 chromosomal region. ABA93767 to ABA93843 and ABB05730 to ABB05745 represent sequences used in the exemplification of the present invention

Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 5; Length 330;

Best Local Similarity 97.9%; Pred. No. 1.7e-122;

Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTPFAVLQSS 60

1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTPFAVLQSS 60

61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELGG 120

61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELGG 120

121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTRPREQYN 180

121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTRPREQYN 180

181 STYRVSVLTVLHQNMWNGKEYCKVSKNKAAPAEIKTISKAKVQPREPQVYTLPPSRDE 240

181 STYRVSVLTVLHQDNLNGKEYCKVSKNKAAPAEIKTISKAKVQPREPQVYTLPPSRDE 240

241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPTPLDSDVSGSFYSLKLTVDKSRW 300

241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPTPLDSDVSGSFYSLKLTVDKSRW 300

QY 301 QQGNVFCSSVMHEALHNHYQOQSLSLSPGK 330

Db 301 QQGNVFCSSVMHEALHNHYQOQSLSLSPGK 330

RESULT 7

ABP71856

ID ABP71856 standard; protein; 330 AA.

XX

AC ABP71856;

XX

DT 17-APR-2003 (first entry)

XX

DE Human IgG1 Fc gamma region.

XX

KW Human; fusion protein; IGE Fc epsilon; IGE Fc gamma; Fc epsilonRI; allergy; Fc epsilonRII; Fc gammaRII; protein therapy; IGE; IGE; asthma; hay fever; allergic asthma; allergic rhinitis; hay fever; food allergy; atopic dermatitis; drug allergy; peanut allergen.

XX

OS Homo sapiens.

XX

PH Key Location/Qualifiers

FT Region 1..98

FT Region /label= CH1 region

FT Region 99..113

FT Region /label= Hinge region

FT Region 114..223

FT Region /label= CH2 region

FT Region 224..330

FT Region /label= CH3 region

XX WO2002102320-A2.

XX

PD 27-DEC-2002.

XX

PF 14-JUN-2002; 2002WO-US019448.

XX

PR 15-JUN-2001; 2001US-0298710P.

XX

PA (TANO-) TANOX INC.

XX

PI An L, Wu H, Fung MSC;

XX

DR WPI; 2003-167440/16.

XX

PT New fusion protein which binds to Fc epsilonRI or RII receptor and Fc gammaRII; receptor, useful for treating or preventing allergies and asthma, comprises an IGE Fc epsilon fragment and an IGE Fc gamma fragment.

PT

PS Disclosure; Fig 5; 32pp; English.

XX

CC The invention relates to a novel fusion protein comprising an IGE Fc epsilon fragment and an IGE Fc gamma fragment, which binds to an Fc epsilonRI and/or Fc epsilonRII receptor and an Fc gammaRII receptor. The fusion protein of the invention may have a use in protein therapy. The fusion protein is useful in treating or preventing IGE-mediated allergies and asthma, such as allergic asthma, allergic rhinitis, hay fever, food allergy, atopic dermatitis and drug allergy. The allergic response is particularly caused by peanut allergen. The present sequence represents the human IgG1 Fc gamma fragment

XX

SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;

Best Local Similarity 97.9%; Pred. No. 1.7e-122;

Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTPFAVLQSS 60

1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTPFAVLQSS 60

61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELGG 120

61 GLYSLSSVVTVPSSSLGTQTYICNVNHKPSNTKVDKVEPKSCDKTHTCPPCPAPELGG 120

Db 61 GLYSLSSVVTVPSSSLGTQYICNVNHPKNTVDKRVKPKSCDKTHTCPCPAPELGG 120  
 QY 121 PSVFLFPKPKDITLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
 Db 121 PSVFLFPKPKDITLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
 QY 131 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 Db 181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 300  
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 300  
 QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330  
 Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 8  
 AAE32915  
 ID AAE32915 standard; protein; 330 AA.  
 AC AAE32915;  
 XX  
 XX  
 DT 24-MAR-2003 (first entry)  
 DE Human immunoglobulin G1 (IgG1) heavy chain Fc region.  
 XX  
 KW T-cell; immunogenic; therapy; human; immunoglobulin G1; IgG1;  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200279232-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 30-MAR-2002; 2002WO-US009815.  
 XX  
 PR 30-MAR-2001; 2001US-0280625P.  
 XX  
 PA (LEXI-) LEXIGEN PHARM CORP.  
 XX  
 PI Gillies SD;  
 XX  
 DR WPI; 2003-103259/09.  
 XX

Reducing the immunogenicity of a fusion protein comprises changing an amino acid within the junction region to reduce the ability of the candidate T-cell epitope identified within the junction spanning to interact with T-cell receptor.  
 XX  
 PS Disclosure; Page 49-50; 68pp; English.  
 XX  
 CC The invention relates to a method for reducing the immunogenicity of a fusion protein which involves identifying a candidate T-cell epitope within a junction spanning a fusion junction of a fusion protein, and changing an amino acid within the junction region to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor. The method is useful for reducing the immunogenicity of a fusion protein. It is useful for analysing, changing or modifying one or more amino acids in the junction region of a fusion protein to identify a T-cell epitope and reduce its ability to interact with a T-cell receptor. The less immunogenic fusion proteins are useful in providing therapeutic treatment. The present sequence is human immunoglobulin G1 (IgG1) heavy chain Fc region used to illustrate the method of the invention  
 XX  
 SQ Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 1.7e-122;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTSMNSGALTSGVHTFPAVLQSS 60  
 Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPVTSMNSGALTSGVHTFPAVLQSS 60  
 QY 61 GLYSLSVVTVPSSSLGTQYICNVNHPKNTVDKRVKPKSCDKTHTCPCPAPELGG 120  
 Db 61 GLYSLSVVTVPSSSLGTQYICNVNHPKNTVDKRVKPKSCDKTHTCPCPAPELGG 120  
 QY 121 PSVFLFPKPKDITLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
 Db 121 PSVFLFPKPKDITLMIISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
 QY 181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 Db 181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 300  
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 300  
 QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330  
 Db 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 9  
 AAE32627  
 ID AAE32627 standard; protein; 330 AA.  
 AC AAE32627;  
 XX  
 XX  
 DT 24-MAR-2003 (first entry)  
 DE Human immunoglobulin G1 (IgG1) heavy chain Fc region.  
 XX  
 KW Human; immunogenic; therapy; immunoglobulin G1; IgG1.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO200279415-A2.  
 XX  
 PD 10-OCT-2002.  
 XX  
 PF 29-MAR-2002; 2002WO-US009650.  
 XX  
 PR 30-MAR-2001; 2001US-0280625P.  
 XX  
 PA (LEXI-) LEXIGEN PHARM CORP.  
 XX  
 PI Gillies SD;  
 XX  
 DR WPI; 2003-111794/10.  
 XX

Reducing the immunogenicity of a fusion protein by changing an amino acid within the junction region spanning a fusion junction of a fusion protein to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor.  
 XX  
 PS Disclosure; Page 49-50; 67pp; English.  
 XX  
 CC The present invention relates to a method of reducing the immunogenicity of a fusion protein. The method involves identifying a candidate T-cell epitope within a junction region spanning a fusion junction of a fusion protein and changing an amino acid within the junction region to reduce the ability of the candidate T-cell epitope to interact with a T-cell receptor. The method is useful for reducing the immunogenicity of fusion proteins for use in therapy. The present sequence is human immunoglobulin G1 (IgG1) heavy chain Fc region. This sequence is used to illustrate the method of the invention  
 XX  
 SQ Sequence 330 AA;



Query Match 98.0%; Score 1729; DB 6; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.7e-122; Indels 0; Gaps 0;  
Matches 323; Conservative 3; Mismatches 4;  
1 ASTKGPSVFPPLAPSSKTSGGTAAALGCLVXDYFPEPVTVSWNSGALTSVHTFPVAVLQSS 60  
1 ASTKGPSVFPPLAPSSKTSGGTAAALGCLVXDYFPEPVTVSWNSGALTSVHTFPVAVLQSS 60  
61 GLYLSLSSVTVTPSSSLGTQYICNVNHPKSNKTKVKKVPEKSCDKTHTCPCPAPELIGG 120  
61 GLYLSLSSVTVTPSSSLGTQYICNVNHPKSNKTKVKKVPEKSCDKTHTCPCPAPELIGG 120  
121 PSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
121 PSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
181 STYRVSVLTVLHONWNGKEYCKVKNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240  
181 STYRVSVLTVLHODWNLNGKEYCKVKNKALPAPIEKTISKAKGQPREPVYTLPPSRDE 240  
241 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 300  
241 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 300  
301 QCGNVFSCVMHEALHNYTKQSLSPGK 330  
301 QCGNVFSCVMHEALHNYTKQSLSPGK 330  
SUIT 10  
R82103  
ABR82103 standard; protein; 330 AA.  
ABR82103;  
23-SEP-2003 (first entry)  
Human DR6 related amino acid sequence SEQ ID NO:5.  
Human; DR6; B-cell mediated disease; immunosuppressive; antirheumatic;  
antiarthritic; antiasthmatic; dermatological; antiinflammatory;  
antipsoriatic; antidiabetic; cytostatic; neuroprotective; thyromimetic;  
antithyroid; nephrotropic; antiinfertility; vasotrophic; virucide;  
hepatotropic; antibacterial; antiulcer; haemostatic; antianaemic;  
antimicrobial; anti-HIV; DR6 agonist; DR6 antagonist; immunity.  
Homo sapiens.  
WO2003051290-A2.  
26-JUN-2003.  
10-DEC-2002; 2002WO-US037596.  
17-DEC-2001; 2001US-0342632P.  
(ELIL) LILLY & CO ELI.  
Liu J, Na S, Song HY, Yang D;  
WPI; 2003-541604/51.  
Treating or preventing a B cell mediated condition e.g., chronic  
hepatitis or chronic cirrhosis, in a mammal by administering a  
pharmaceutical composition comprising a DR6 agonist or DR6 antagonist to  
the mammal.  
Disclosure; Page 96-97; 97pp; English.  
The present invention describes a method (M1) for treating or preventing  
a B cell mediated condition in a mammal by administering a pharmaceutical  
composition comprising a DR6 agonist or DR6 antagonist to the mammal.  
Also described: (1) inhibiting B cell mediated immunity in a mammal, by

administering a pharmaceutical composition comprising at least one DR6  
agonist; (2) use of a DR6 agonist in the manufacture of a medicament for  
treating or preventing at least one symptom associated with conditions  
(C1) such as aberrant apoptosis, graft-versus-host disease (GVHD), atopy,  
rheumatoid arthritis, asthma, eczema, inflammatory bowel disease, cancer,  
vasculitis, psoriasis, insulin-dependent diabetes mellitus, pancreatitis,  
psoriasis, multiple sclerosis, Hashimoto's thyroiditis, Graves' disease,  
transplant rejection, systemic lupus erythematosus, Behcet's disease,  
autoimmune nephropathy, autoimmune haematopathy, idiopathic interstitial  
pneumonia, hypersensitivity pneumonitis, autoimmune dermatosis,  
autoimmune cardiopathy, autoimmune infertility, autoimmune gastritis,  
fibrosing lung disease, fulminant viral hepatitis B, fulminant viral  
hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis,  
Helicobacter pylori-associated ulceration, organ rejection after  
transplantation, chronic glomerulonephritis, thrombotic thrombocytopenic  
purpura (TTP) and haemolytic uraemic syndrome (HUS), aplastic anaemia,  
myelodysplasia, multiple organ dysfunction syndrome (MDS), adult  
respiratory distress syndrome (ARDS), and at least one condition or  
symptom related to the conditions, in a mammal; and (3) use of DR6  
antagonist in the manufacture of a medicament for treating or preventing  
at least one symptom associated with conditions (C2) such as aberrant  
apoptosis, immunodeficiency, bacterial infection, viral infection,  
microbial infection, complications of infection, HIV, HIV-induced  
lymphoma, HIV-induced AIDS, fulminant viral hepatitis B, fulminant viral  
hepatitis C, autoimmune hepatitis, chronic hepatitis, chronic cirrhosis,  
recuperation from chemotherapy, recuperation from irradiation therapy, in a  
mammal. DR6 has immunosuppressive, antirheumatic, antiarthritic,  
antiasthmatic, dermatological, antiinflammatory, antipsoriatic,  
nephrotropic, cytostatic, neuroprotective, thyromimetic, antithyroid,  
antibacterial, antiulcer, haemostatic, antianaemic, antimicrobial and  
anti-HIV activities. (M1) is useful for treating or preventing at least  
one symptom associated with (C1) in a mammal, preferably human, by  
administering DR6 agonist, and for treating or preventing at least one  
symptom associated with (C2) by administering DR6 antagonist. The present  
sequence represents a human DR6 related amino acid sequence, which is  
given in the exemplification of the present invention  
XX Sequence 330 AA;  
SQ  
Query Match 98.0%; Score 1729; DB 6; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.7e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 ASTKGPSVFPPLAPSSKTSGGTAAALGCLVXDYFPEPVTVSWNSGALTSVHTFPVAVLQSS 60  
DB 1 ASTKGPSVFPPLAPSSKTSGGTAAALGCLVXDYFPEPVTVSWNSGALTSVHTFPVAVLQSS 60  
QY 61 GLYLSLSSVTVTPSSSLGTQYICNVNHPKSNKTKVKKVPEKSCDKTHTCPCPAPELIGG 120  
DB 61 GLYLSLSSVTVTPSSSLGTQYICNVNHPKSNKTKVKKVPEKSCDKTHTCPCPAPELIGG 120  
QY 121 PSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
DB 121 PSVFLFPPKPKDITLMI SRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
QY 181 STYRVSVLTVLHONWNGKEYCKVKNKALPAPIEKTISKAKVQPREPVYTLPPSRDE 240  
DB 181 STYRVSVLTVLHODWNLNGKEYCKVKNKALPAPIEKTISKAKGQPREPVYTLPPSRDE 240  
QY 241 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 300  
DB 241 LTKQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPPVLDSDGSFFLYSKLTVDKSRW 300  
QY 301 QCGNVFSCVMHEALHNYTKQSLSPGK 330  
DB 301 QCGNVFSCVMHEALHNYTKQSLSPGK 330  
RESULT 11  
AA031102

ID AAO31102 standard; protein; 330 AA.  
 AC AAO31102;  
 XX  
 DT 06-OCT-2003 (first entry)  
 XX  
 DE Human A2-G8 SCF antibody heavy chain constant region.  
 XX  
 KW Human; antibody; stem cell factor; mast cell growth factor; asthma; SCF;  
 KW steel factor; c-kit ligand; gene therapy; heavy chain.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2003051311-A2.  
 XX  
 PD 26-JUN-2003.  
 XX  
 PF 16-DEC-2002; 2002WO-US040227.  
 XX  
 PR 17-DEC-2001; 2001US-0342174P.  
 XX  
 PA (FARB ) BAYER CORP.  
 XX  
 PI Takeuchi T, Tomkinson A, Neben S;  
 XX  
 DR WPI; 2003-523500/49.  
 DR N-PSDB; AAL62618.  
 XX  
 PT New purified human antibody that binds to stem cell factor protein,  
 PT useful for preparing a composition for treating asthma.  
 XX  
 PS Example 10; Page 47-48; 94pp; English.  
 XX  
 CC The invention provides human antibodies that bind to stem cell factor  
 CC (SCF) protein. SCF is also known as mast cell growth factor, steel factor  
 CC or c-kit ligand. Antibodies of the invention are useful for preparing  
 CC compositions for treating asthma. They are also used in gene therapy. The  
 CC present sequence is human SCF antibody heavy chain constant region  
 XX  
 SQ Sequence 330 AA;  
 Query Match 98.0%; Score 1729; DB 6; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 1.7e-122;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 DB 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 QY 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHTCPPCPAPPELLGG 120  
 DB 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHTCPPCPAPPELLGG 120  
 QY 121 PSVFLPPPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNVKTKPREEQYN 180  
 DB 121 PSVFLPPPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNVKTKPREEQYN 180  
 QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 DB 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300  
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300  
 QY 301 QQQNVFSCSVMEALHHNHYTKQKLSLSPGK 330  
 DB 301 QQQNVFSCSVMEALHHNHYTKQKLSLSPGK 330  
 RESULT 12  
 ABR55836  
 ID ABR55836 standard; protein; 330 AA.

XX ABR55836;  
 AC  
 DT 02-SEP-2003 (first entry)  
 XX  
 DE Anti-Ang-2 antibody IgG1 constant region.  
 XX  
 KW Ang-2; angiotensin-2; anorectic; cytostatic; antiarteriosclerotic;  
 KW gynaecological; antiinflammatory; osteopathic; antipsoriatic; cancer;  
 KW angiogenesis; antibody; human.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO2003030833-A2.  
 XX  
 PD 17-APR-2003.  
 XX  
 PF 11-OCT-2002; 2002WO-US032613.  
 XX  
 PR 11-OCT-2001; 2001US-0328604P.  
 PR 10-OCT-2002; 2002US-00269805.  
 XX  
 PA (AMGE-) AMGEN INC.  
 XX  
 PI Oliner JD;  
 XX  
 DR WPI; 2003-504963/47.  
 XX  
 PT New specific binding agents (i.e. anti-Angiotensin-2 antibodies), useful  
 PT for inhibiting undesired angiogenesis, or treating e.g. cancers, obesity,  
 PT hemangioma, arteriosclerosis, atherosclerosis or endometriosis.  
 XX  
 PS Example 4; Page 96; 161pp; English.  
 XX  
 CC The invention relates to a specific binding agent, which comprises at  
 CC least one peptide selected from any of 62 peptides (ABR55769-830) or its  
 CC fragment. The binding agents are antibodies that recognize and bind to  
 CC angiotensin-2 (Ang-2). The specific binding agent, particularly the  
 CC antibody, is useful for inhibiting undesired angiogenesis, treating  
 CC cancers, inhibiting undesired angiogenesis, modulating or inhibiting Ang-  
 CC 2 activity, modulating vascular permeability or plasma leakage, or  
 CC treating a disease (e.g. ocular neovascular disease, obesity,  
 CC haemangioblastoma, haemangioma, arteriosclerosis, inflammatory disease,  
 CC inflammatory disorders, atherosclerosis, endometriosis, neoplastic  
 CC disease, bone-related disease, or psoriasis) in a mammal. The present  
 CC sequence represents a human IgG1 constant region of an anti-Ang-2  
 CC antibody  
 XX  
 SQ Sequence 330 AA;  
 Query Match 98.0%; Score 1729; DB 6; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 1.7e-122;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 DB 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 QY 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHTCPPCPAPPELLGG 120  
 DB 61 GLYSLSSVTVTPSSSLGTQYICNVNHPKSTKVDKKVEPKSCDKTHTCPPCPAPPELLGG 120  
 QY 121 PSVFLPPPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNVKTKPREEQYN 180  
 DB 121 PSVFLPPPKPKDILMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHNVKTKPREEQYN 180  
 QY 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 DB 181 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300  
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSLKLTVDKSRW 300

301 QQGNVFCSCVMHEALHNHYQQRSLSPGK 330  
301 QQGNVFCSCVMHEALHNHYQQRSLSPGK 330

RESULT 13  
AAO30893 standard; protein; 330 AA.

AAO30893;  
22-SEP-2003 (first entry)

Human immunoglobulin gamma (IgG) 1 constant region.

Cytokine; interleukin-2; IL-2; cancer; viral infection; immune disorder;  
gene therapy; immunoglobulin; Ig; human.

Homo sapiens.

WO2003048334-A2.

12-JUN-2003.

04-DEC-2002; 2002WO-US038780.

04-DEC-2001; 2001US-0337113P.

12-APR-2002; 2002US-0371966P.

(EMDL-) EMD LEXIGEN RES CENT CORP.

Gillies SD;

WPI; 2003-513757/48.

New fusion protein comprising a non-IL-2 moiety fused to a mutant IL-2 moiety, useful for preparing a composition for treating cancer, viral infections or immune disorders.

Example 1; Page 51-53; 71pp; English.

The invention relates to cytokine fusion proteins with increased therapeutic index and methods for increasing the therapeutic index of such fusion proteins. The fusion protein comprises a non-interleukin-2 (IL-2) moiety fused to a mutant IL-2 moiety. It is useful for preparing a composition for treating cancer, viral infections or immune disorders. The fusion protein is also used in gene therapy. The present sequence is human immunoglobulin gamma (IgG) constant region. This sequence is used to illustrate the method of the invention

Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 6; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.7e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

61 GLYSLSVVTVPSLSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120

61 GLYSLSVVTVPSLSLGTQTYICNVNHPKSNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120

121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMTYVDGVEVHNKTKPREEQYN 180

121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNMTYVDGVEVHNKTKPREEQYN 180

181 STYRVSVLTVLHQWMNCKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

181 STYRVSVLTVLHQWMNCKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

QY 241 LTRKQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGVSGFSLYSLTVDKSRW 300  
DB 241 LTRKQVSLTCLVKGFYPSDIAVWESNGQPENNYKTTPPVLDSDGVSGFSLYSLTVDKSRW 300  
QY 301 QQGNVFCSCVMHEALHNHYQQRSLSPGK 330  
DB 301 QQGNVFCSCVMHEALHNHYQQRSLSPGK 330

RESULT 14

ADFL11389  
ID ADF11389 standard; protein; 330 AA.

XX ADF11389;

XX 12-FEB-2004 (first entry)

Anti-OPGL antibody heavy chain constant region SEQ ID NO:2.

human; antibody; osteoprotegerin ligand; OPGL; osteopenic disorder;  
osteoarthritic; cytostatic; gene therapy; bone disorder;  
osteoporosis; bone loss; arthritis; Paget's disease; osteopenia.

OS Homo sapiens.

PN WO2003086289-A2.

XX 23-OCT-2003.

XX 07-APR-2003; 2003WO-US010749.

XX 05-APR-2002; 2002US-0370407P.

XX (AMGE-) AMGEN INC.

XX Boyle WJ, Medlock E, Sullivan JK, Elliott RL, Martin F, Huang H;

XX WPI; 2003-845253/78.

XX N-PSDB; ADF11389.

XX New isolated antibody that specifically binds osteoprotegerin ligand,  
useful for diagnosing or treating bone disorders, such as osteoporosis,  
bone loss from arthritis, Paget's disease or osteopenia.

XX Example 3; SEQ ID NO 2; 156pp; English.

The present invention describes an isolated human antibody (I) that specifically binds osteoprotegerin ligand (OPGL). Also described: (1) a pharmaceutical composition comprising a pharmaceutical carrier and a therapeutic amount of (I); (2) methods of treating an osteopenic disorder in a patient, comprising administering to a patient the pharmaceutical composition of (I) or a pharmaceutical amount of (I); and (3) a method for detecting OPGL in a biological sample, comprising contacting the sample with (I) under conditions that allow for binding of the antibody to OPGL, and measuring the level of bound antibody in the sample. (I) has osteopathic, antiarthritic and cytostatic activities, and can be used in gene therapy. The composition and methods are useful in diagnosing or treating bone disorders, such as osteoporosis, bone loss from arthritis, Paget's disease or osteopenia. The antibody (I) may also be used for detecting OPGL in biological samples and in identifying cells or tissues that produce the protein. The present sequence represents a sequence which is used in the exemplification of the present invention.

XX Sequence 330 AA;

Query Match 98.0%; Score 1729; DB 7; Length 330;  
Best Local Similarity 97.9%; Pred. No. 1.7e-122;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

DB 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPPELLGG 120  
 DB 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPPELLGG 120  
 QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
 DB 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
 QY 181 STYRVSVLTVLHQNWMNGKEYKCVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 DB 181 STYRVSVLTVLHQNWMNGKEYKCVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYSLYSLTVDKSRW 300  
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYSLYSLTVDKSRW 300  
 QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330  
 DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

RESULT 15

ADE97351  
 ID ADE97351 standard; protein; 330 AA.  
 AC ADE97351;  
 XX  
 DT 12-FEB-2004 (first entry)  
 XX  
 DE Human IgG1 heavy chain constant region protein - SEQ ID 20.  
 XX  
 KW immunoadhesin; immunoglobulin heavy chain; J chain; joining; toxin;  
 KW virucide; antibacterial; anthrax; rhinovirus infection; common cold;  
 KW intercellular adhesion molecule; ICAM-1; human; constant region; IGG.  
 XX  
 OS Homo sapiens.  
 XX  
 PN WO2003064992-A2.  
 XX  
 PD 07-AUG-2003.  
 XX  
 PF 25-OCT-2002; 2002WO-US034197.  
 XX  
 PR 26-OCT-2001; 2001US-00047542.  
 XX  
 PA (PLAN-) PLANET BIOTECHNOLOGY INC.  
 PA (LARR/) LARRICK J W.  
 PA (WYCO/) WYCOFF K L.  
 XX  
 PI Larrick JW, Wycoff KL;  
 XX  
 WP1; 2003-636816/60.  
 DR N-PSDB; ADE97350, ADE97376.  
 XX  
 XX New immunoadhesin, useful for treating anthrax and rhinovirus, comprises  
 PT chimeric toxin receptor protein linked to immunoglobulin heavy chain, and  
 PT J chain and secretory component associated with the chimeric toxin  
 PT receptor protein.  
 XX  
 PS Disclosure; SEQ ID NO 20; 288pp; English.  
 XX  
 CC The invention relates to a novel immunoadhesin comprising a chimeric  
 CC toxin receptor protein consisting of a toxin receptor protein linked to  
 CC at least a portion of an immunoglobulin heavy chain with a J (joining)  
 CC chain and secretory component (SC) associated with the chimeric toxin  
 CC receptor protein. The immunoadhesin comprises a chimeric bacterial or  
 CC viral toxin receptor protein and the immunoadhesin has plant-specific  
 CC glycosylation. The immunoadhesin of the invention demonstrates virucide  
 CC and antibacterial activities and may be useful for reducing the binding  
 CC of a viral or bacterial antigen to a host cell and thus for treating or  
 CC preventing anthrax, as well as human rhinovirus infection which results  
 CC in the common cold. The current sequence is that of the human  
 CC immunoadhesin-related protein of the invention.

XX SQ Sequence 330 AA;  
 Query Match 98.0%; Score 1729; DB 7; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 1.7e-122;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ASTKGSPVPLAPSSKSTSGGTAALGCLVKDYFPPVTVSVNSGALTSGVHTFPAVLOSS 60  
 DB 1 ASTKGSPVPLAPSSKSTSGGTAALGCLVKDYFPPVTVSVNSGALTSGVHTFPAVLOSS 60  
 QY 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPPELLGG 120  
 DB 61 GLYSLSVVTVFSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPCPAPPELLGG 120  
 QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
 DB 121 PSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
 QY 181 STYRVSVLTVLHQNWMNGKEYKCVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 DB 181 STYRVSVLTVLHQNWMNGKEYKCVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYSLYSLTVDKSRW 300  
 DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYSLYSLTVDKSRW 300  
 QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330  
 DB 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330

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GenCore version 5.1.6  
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- 19: /cgn2\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pep.\*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

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4	1729	98.0	330	10	US-09-892-949-38
5	1729	98.0	330	13	US-10-047-542-20
6	1729	98.0	330	14	US-10-269-805-68
7	1729	98.0	330	14	US-10-310-719-8
8	1729	98.0	330	14	US-10-112-562-1
9	1729	98.0	330	14	US-10-320-231A-81
10	1729	98.0	330	14	US-10-383-902A-6
11	1729	98.0	330	15	US-10-408-901-2
12	1729	98.0	330	15	US-10-420-034A-15
13	1729	98.0	330	15	US-10-257-907-5

14	1729	98.0	330	15	US-10-656-769-2	Sequence 2, Appli
15	1729	98.0	330	16	US-10-772-531-38	Sequence 38, Appli
16	1729	98.0	330	17	US-10-479-326-1	Sequence 1, Appli
17	1729	98.0	330	10	US-09-990-586-98	Sequence 98, Appli
18	1729	98.0	332	14	US-10-310-113-167	Sequence 167, App
19	1729	98.0	332	14	US-10-230-880-98	Sequence 98, Appli
20	1729	98.0	333	15	US-10-272-899A-8	Sequence 8, Appli
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## ALIGNMENTS

### RESULT 1

US-09-847-208-2  
; Sequence 2, Application US/09847208  
; Publication No. US20030082190A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; APPLICANT: Zhang, Ke  
; APPLICANT: Zhu, Daocheng  
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF  
; FILE REFERENCE: UC67.002A  
; CURRENT FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 177  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 2  
; LENGTH: 330  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-847-208-2

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; Sequence 2, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; FILE REFERENCE: UC067, 004A
; CURRENT APPLICATION NUMBER: US/10/000, 439
; CURRENT FILING DATE: 2001-10-24
; PRIOR APPLICATION NUMBER: US 09/847, 208
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-2

Query Match 100.0%; Score 1764; DB 14; Length 330;
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DB 61 GLYSLSSVTVFSSSLGTQYICNVNHRPSNTKVDKVEPKSCDKHTHTCPPCPAPELGG 120
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DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFFLYSLKLTVDKSRW 300
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DB 301 QQGNVFCSCVMHEALHNYHQORSLSLSPGK 330

RESULT 3
US-09-995-898A-15
; Sequence 15, Application US/09995898A
; Publication No. US20030027253A1
; GENERAL INFORMATION:
; APPLICANT: Presnell, Scott R.
; APPLICANT: Xu, Wenfeng
; APPLICANT: No. US20030027253A1ak, Julia E.
; APPLICANT: Whitmore, Theodore E.

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; APPLICANT: Grant, Francis J.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR19
; FILE REFERENCE: 00-108
; CURRENT APPLICATION NUMBER: US/09/995,898A
; CURRENT FILING DATE: 2001-11-28
; PRIOR APPLICATION NUMBER: US 60/253,561
; PRIOR FILING DATE: 2000-11-28
; PRIOR APPLICATION NUMBER: US 60/267,211
; PRIOR FILING DATE: 2001-02-07
; NUMBER OF SEQ ID NOS: 50
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 15
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-995-898A-15

Query Match 98.0%; Score 1729; DB 10; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.4e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
QY 61 GLYSLSSVTVFSSSLGTQYICNVNHRPSNTKVDKVEPKSCDKHTHTCPPCPAPELGG 120
DB 61 GLYSLSSVTVFSSSLGTQYICNVNHRPSNTKVDKVEPKSCDKHTHTCPPCPAPELGG 120
QY 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
DB 121 PSVFLPPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPRREQYN 180
QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFFLYSLKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVGFFLYSLKLTVDKSRW 300
QY 301 QQGNVFCSCVMHEALHNYHQORSLSLSPGK 330
DB 301 QQGNVFCSCVMHEALHNYHQORSLSLSPGK 330

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RESULT 4
US-09-892-949-38
; Sequence 38, Application US/09892949
; Publication No. US20030096339A1
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Gao, Zeren
; APPLICANT: Whitmore, Theodore E.
; APPLICANT: Kuiper, Joseph L.
; APPLICANT: Maurer, Mark F.
; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17
; FILE REFERENCE: 00-42
; CURRENT APPLICATION NUMBER: US/09/892,949
; CURRENT FILING DATE: 2001-06-26
; PRIOR APPLICATION NUMBER: US 60/214,282
; PRIOR FILING DATE: 2000-06-26
; PRIOR APPLICATION NUMBER: US 60/214,955
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 60/267,963
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 93
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 38
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens

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-09-892-949-38

Query Match 98.0%; Score 1729; DB 10; Length 330;  
Best Local Similarity 97.9%; Pred. No. 6.4e-126;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
  
61 GLYSLSVTVTPSSSLGTQYICNVNHPKSNKALPAPIEKTSKAKVQPREPQVYTLPPSRDE 120  
61 GLYSLSVTVTPSSSLGTQYICNVNHPKSNKALPAPIEKTSKAKVQPREPQVYTLPPSRDE 120  
  
121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNKTKPREEQYN 180  
121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNKTKPREEQYN 180  
  
181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTSKAKVQPREPQVYTLPPSRDE 240  
181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTSKAKVQPREPQVYTLPPSRDE 240  
  
241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 300  
241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 300  
  
301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330  
301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 5  
US-10-047-542-20  
Sequence 20, Application US/10047542  
Publication No. US20020168367A1  
GENERAL INFORMATION:  
APPLICANT: LARRICK, JAMES W.  
APPLICANT: WYCOFF, KEITH L.  
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL  
TITLE OF INVENTION: NOVEL IMMUNOADHESINS FOR TREATING AND PREVENTING VIRAL  
FILE REFERENCE: 030905.0004.CIP1  
CURRENT APPLICATION NUMBER: US/10/047.542  
CURRENT FILING DATE: 2001-10-26  
PRIOR APPLICATION NUMBER: PCT/US01/13932  
PRIOR FILING DATE: 2001-04-28  
PRIOR APPLICATION NUMBER: 60/200,298  
PRIOR FILING DATE: 2000-04-28  
NUMBER OF SEQ ID NOS: 101  
SOFTWARE: PatentIn Ver. 2.1  
SEQ ID NO 20  
LENGTH: 330  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-047-542-20

Query Match 98.0%; Score 1729; DB 13; Length 330;  
Best Local Similarity 97.9%; Pred. No. 6.4e-126;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
  
61 GLYSLSVTVTPSSSLGTQYICNVNHPKSNKALPAPIEKTSKAKVQPREPQVYTLPPSRDE 120  
61 GLYSLSVTVTPSSSLGTQYICNVNHPKSNKALPAPIEKTSKAKVQPREPQVYTLPPSRDE 120  
  
121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNKTKPREEQYN 180  
121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNKTKPREEQYN 180  
  
181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTSKAKVQPREPQVYTLPPSRDE 240  
181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTSKAKVQPREPQVYTLPPSRDE 240

Db 181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTSKAKVQPREPQVYTLPPSRDE 240  
Qy 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 300  
Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 300  
Qy 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330  
Db 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330  
  
RESULT 6  
US-10-269-805-68  
Sequence 68, Application US/10269805  
Publication No. US20030124129A1  
GENERAL INFORMATION:  
APPLICANT: OLINER, JONATHAN D.  
TITLE OF INVENTION: ANGIOPOIETIN-2 SPECIFIC BINDING AGENTS  
FILE REFERENCE: A-722  
CURRENT APPLICATION NUMBER: US/10/269,805  
CURRENT FILING DATE: 2002-10-10  
PRIOR APPLICATION NUMBER: US 60/328,604  
PRIOR FILING DATE: 2001-10-11  
NUMBER OF SEQ ID NOS: 76  
SOFTWARE: PatentIn version 3.1  
SEQ ID NO 68  
LENGTH: 330  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-269-805-68

Query Match 98.0%; Score 1729; DB 14; Length 330;  
Best Local Similarity 97.9%; Pred. No. 6.4e-126;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
  
61 GLYSLSVTVTPSSSLGTQYICNVNHPKSNKALPAPIEKTSKAKVQPREPQVYTLPPSRDE 120  
61 GLYSLSVTVTPSSSLGTQYICNVNHPKSNKALPAPIEKTSKAKVQPREPQVYTLPPSRDE 120  
  
121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNKTKPREEQYN 180  
121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVVHNKTKPREEQYN 180  
  
181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTSKAKVQPREPQVYTLPPSRDE 240  
181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTSKAKVQPREPQVYTLPPSRDE 240  
  
241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 300  
241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDSDGSGFFLYSKLTVDKSRW 300  
  
301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330  
301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 7  
US-10-310-719-8  
Sequence 8, Application US/10310719  
Publication No. US20030166163A1  
GENERAL INFORMATION:  
APPLICANT: GILLIES, STEPHEN  
TITLE OF INVENTION: Immunocytokines With Modulated Selectivity  
FILE REFERENCE: LEX-020  
CURRENT APPLICATION NUMBER: US/10/310,719  
CURRENT FILING DATE: 2002-12-04  
PRIOR APPLICATION NUMBER: 60/337,113  
PRIOR FILING DATE: 2001-12-04  
PRIOR APPLICATION NUMBER: 60/371,966

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; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 8
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc
; LOCATION: (1)..(330)
; OTHER INFORMATION: IgG1 constant region
US-10-310-719-8

Query Match          98.0%; Score 1729; DB 14; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.4e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120
DB 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120

QY 121 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

QY 181 STYRVSVLTVLHQNWNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQNWNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300

QY 301 QQGNVFSCVMHEALHNHYQOQSLSLSPGK 330
DB 301 QQGNVFSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 9
US-10-320-231A-81
; Sequence 81, Application US/10320231A
; Publication No. US20030194405A1
; GENERAL INFORMATION:
; APPLICANT: Neben, Steven
; APPLICANT: Takeuchi, Toshihiko
; APPLICANT: Tomkinson, Adrian
; TITLE OF INVENTION: Antibody Inhibiting Stem Cell Factor Activity And Use For
; TITLE OF INVENTION: Treatment Of Asthma
; FILE REFERENCE: 7430*163
; CURRENT APPLICATION NUMBER: US/10/320,231A
; PRIOR FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: US 60/342,174
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 81
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-320-231A-81

Query Match          98.0%; Score 1729; DB 14; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.4e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60

QY 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120
DB 61 GLYSLSVVTVPPSSSLGTQTYICNVNHPKSNKTKVDKVEPKSCDKHTHTCPPCPAPPELLGG 120

QY 121 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 121 PSVFLFPPPKPDKTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180

QY 181 STYRVSVLTVLHQNWNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 181 STYRVSVLTVLHQNWNGKEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300
DB 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDSDGSGFFLYSKLTVDKSRW 300

QY 301 QQGNVFSCVMHEALHNHYQOQSLSLSPGK 330
DB 301 QQGNVFSCVMHEALHNHYQOQSLSLSPGK 330

US-10-112-582-1
; Sequence 1, Application US/10112582
; Publication No. US20030166877A1
; GENERAL INFORMATION:
; APPLICANT: Gillies, Stephen
; TITLE OF INVENTION: Reducing the Immunogenicity of Fusion Proteins
; FILE REFERENCE: LEX-017
; CURRENT APPLICATION NUMBER: US/10/112,582
; CURRENT FILING DATE: 2002-03-29
; PRIOR APPLICATION NUMBER: US 60/280,625
; PRIOR FILING DATE: 2001-03-30
; NUMBER OF SEQ ID NOS: 59
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 1
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: misc
; OTHER INFORMATION: human Ig gamma heavy chain C region
US-10-112-582-1

Query Match          98.0%; Score 1729; DB 14; Length 330;
Best Local Similarity 97.9%; Pred. No. 6.4e-126;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
DB 1 ASTKGPSVFPPLAPSSKSTGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
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SULT 10  
-10-383-902A-6  
Sequence 5, Application US/10383902A  
Publication No. US200400224408A1  
GENERAL INFORMATION:  
APPLICANT: Hoogenboom, Henricus Renerus Jacobus Mattheus  
APPLICANT: Mullberg, Jurgan  
APPLICANT: Ladner, Robert C.  
TITLE OF INVENTION: LIGAND SCREENING AND DISCOVERY  
FILE REFERENCE: 10280-042001  
CURRENT APPLICATION NUMBER: US/10/383,902A  
CURRENT FILING DATE: 2003-03-07  
PRIOR APPLICATION NUMBER: US 60/362,403  
PRIOR FILING DATE: 2002-03-07  
NUMBER OF SEQ ID NOS: 58  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 6  
LENGTH: 330  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: synthetically generated plasmid sequence  
-10-383-902A-6  
Query Match 98.0%; Score 1729; DB 14; Length 330;  
Best Local Similarity 97.9%; Pred. No. 6.4e-126;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
1 ASTKGPSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
1 ASTKGPSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120  
61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120  
121 PSVFLPPPKPDTLMIKSRTPETVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQYN 180  
121 PSVFLPPPKPDTLMIKSRTPETVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQYN 180  
181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240  
181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240  
241 LTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300  
241 LTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300  
301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330  
301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330  
RESULT 11  
-10-408-901-2  
Sequence 2, Application US/10408901  
Publication No. US2004002313A1  
GENERAL INFORMATION:  
APPLICANT: Boyle, William  
APPLICANT: Huang, Haichun  
APPLICANT: Elliot, Robin  
APPLICANT: Sullivan, John  
APPLICANT: Medlock, Eugene  
APPLICANT: Martin, Francis  
TITLE OF INVENTION: Human Anti-OPGL Neutralizing Antibodies As Selective OPGL Pathway  
FILE REFERENCE: MEHB 01-1145-A  
CURRENT APPLICATION NUMBER: US/10/408,901  
CURRENT FILING DATE: 2003-04-07  
NUMBER OF SEQ ID NOS: 76  
SOFTWARE: PatentIn version 3.0  
SEQ ID NO 2  
LENGTH: 330

TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-408-901-2  
Query Match 98.0%; Score 1729; DB 15; Length 330;  
Best Local Similarity 97.9%; Pred. No. 6.4e-126;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
1 ASTKGPSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
1 ASTKGPSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120  
61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120  
121 PSVFLPPPKPDTLMIKSRTPETVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQYN 180  
121 PSVFLPPPKPDTLMIKSRTPETVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQYN 180  
181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240  
181 STYRVSVLTVLHQNWMNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 240  
241 LTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300  
241 LTKQVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTPPVLDSDGSFFLYSKLTVDKSRW 300  
301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330  
301 QQGNVFCSCVMHEALHNHYTQKSLSLSPGK 330  
RESULT 12  
US-10-420-034A-15  
Sequence 15, Application US/10420034A  
Publication No. US20040029228A1  
GENERAL INFORMATION:  
APPLICANT: Xu, Menfeng  
APPLICANT: No. US20040029228A1ak, Julia E.  
APPLICANT: Whitmore, Theodore E.  
APPLICANT: Grant, Francis J.  
APPLICANT: Kindsvogel, Wayne R.  
APPLICANT: Klucher, Kevin M.  
TITLE OF INVENTION: CYTOKINE RECEPTOR  
FILE REFERENCE: 02-10  
CURRENT APPLICATION NUMBER: US/10/420,034A  
CURRENT FILING DATE: 2003-04-18  
PRIOR APPLICATION NUMBER: 60/373,813  
PRIOR FILING DATE: 2002-04-19  
NUMBER OF SEQ ID NOS: 69  
SOFTWARE: FastSeq for Windows Version 4.0  
SEQ ID NO 15  
LENGTH: 330  
TYPE: PRT  
ORGANISM: Homo sapiens  
US-10-420-034A-15  
Query Match 98.0%; Score 1729; DB 15; Length 330;  
Best Local Similarity 97.9%; Pred. No. 6.4e-126;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
1 ASTKGPSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
1 ASTKGPSVFPLAPSSKSTSGTAAALCLVKDYFPEPTVTSWNSGALTSGVHTFPAVLQSS 60  
61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120  
61 GLYSLSSVTVTPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120  
121 PSVFLPPPKPDTLMIKSRTPETVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQYN 180  
121 PSVFLPPPKPDTLMIKSRTPETVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQYN 180

Db 121 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNKATKPREQYN 180  
 QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETKISKAKVQPREPQVYTLPPSRDE 240  
 Db 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETKISKAKVQPREPQVYTLPPSRDE 240  
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 300  
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 300  
 QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330  
 Db 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 13  
 US-10-257-907-5  
 ; Sequence 5, Application US/10257907  
 ; Publication No. US20040043022A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Heuer, Josef  
 ; APPLICANT: Liu, Jinqi  
 ; APPLICANT: Na, Songqing  
 ; APPLICANT: Song, Ho Yeong  
 ; APPLICANT: Yang, Derek Di  
 ; TITLE OF INVENTION: TREATING T-CELL MEDIATED DISEASES BY MODULATING DR6 ACTIVITY  
 ; FILE REFERENCE: X-13992  
 ; CURRENT APPLICATION NUMBER: US/10/257,907  
 ; CURRENT FILING DATE: 2002-10-16  
 ; NUMBER OF SEQ ID NOS: 5  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 5  
 ; LENGTH: 330  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-257-907-5

Query Match 98.0%; Score 1729; DB 15; Length 330;  
 Best Local Similarity 97.9%; Pred. No. 6.4e-126;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 Db 1 ASTKGPSVFPLAPSSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 QY 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELGG 120  
 Db 61 GLYSLSSVTVTPSSSLGTQTYICNVNHKPSNTKVDKKVEPKSCDKTHCTCPCPAPELGG 120  
 QY 121 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNKATKPREQYN 180  
 Db 121 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNKATKPREQYN 180  
 QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETKISKAKVQPREPQVYTLPPSRDE 240  
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 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 300  
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 300  
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 Db 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330

RESULT 14  
 US-10-656-769-2  
 ; Sequence 2, Application US/10656769  
 ; Publication No. US2004009712A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Varnum, Brian  
 ; APPLICANT: Witte, Allison

; APPLICANT: Vezina, Chris  
 ; APPLICANT: Wong, Lu Min  
 ; APPLICANT: Qian, Xueming  
 ; TITLE OF INVENTION: Therapeutic Human Anti-IL-1R Monoclonal Antibody  
 ; FILE REFERENCE: 01.1554  
 ; CURRENT APPLICATION NUMBER: US/10/656,769  
 ; CURRENT FILING DATE: 2003-09-05  
 ; NUMBER OF SEQ ID NOS: 79  
 ; SOFTWARE: Patent in version 3.0  
 ; SEQ ID NO 2  
 ; LENGTH: 330  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens  
 US-10-656-769-2

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 QY 121 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNKATKPREQYN 180  
 Db 121 PSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVVHNKATKPREQYN 180  
 QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETKISKAKVQPREPQVYTLPPSRDE 240  
 Db 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIETKISKAKVQPREPQVYTLPPSRDE 240  
 QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 300  
 Db 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFFLYSKLTVDKSRW 300  
 QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330  
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RESULT 15  
 US-10-772-531-38  
 ; Sequence 38, Application US/10772531  
 ; Publication No. US2004014242A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Sprecher, Candy A.  
 ; APPLICANT: Presnell, Scott R.  
 ; APPLICANT: Gao, Zeren  
 ; APPLICANT: Whitmore, Theodore E.  
 ; APPLICANT: Kuijper, Joseph L.  
 ; APPLICANT: Maurer, Mark F.  
 ; TITLE OF INVENTION: CYTOKINE RECEPTOR ZCYTOR17  
 ; FILE REFERENCE: 00-42  
 ; CURRENT APPLICATION NUMBER: US/10/772,531  
 ; CURRENT FILING DATE: 2004-02-05  
 ; PRIOR APPLICATION NUMBER: US/09/892,949  
 ; PRIOR FILING DATE: 2001-06-26  
 ; PRIOR APPLICATION NUMBER: US 60/214,282  
 ; PRIOR FILING DATE: 2000-06-26  
 ; PRIOR APPLICATION NUMBER: US 60/214,955  
 ; PRIOR FILING DATE: 2000-06-29  
 ; PRIOR APPLICATION NUMBER: US 60/267,963  
 ; PRIOR FILING DATE: 2001-08-02  
 ; NUMBER OF SEQ ID NOS: 93  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 38  
 ; LENGTH: 330  
 ; TYPE: PRT  
 ; ORGANISM: Homo sapiens

-10-772-531-38

Query Match 38.0%; Score 1729; DB 16; Length 330;  
Best Local Similarity 97.9%; Pred. No. 6.4e-126;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
  
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1 ASTKGPVFPPLAPSSKSTSGTAALGCLVKDYPPVTVSWNSGALTSGVHTFPVAVLOSS 60  
|||||  
  
61 GLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKKEPKSCDKTHTCPCPAPPELLGG 120  
|||||  
61 GLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKKEPKSCDKTHTCPCPAPPELLGG 120  
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121 PSVFLFPKPKDITLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVHNAKTKPREEQYN 180  
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241 LTKQVSLTCLVKGFPYSDIAVESNGQPENNYKTTTPVLDSDGSEFFLYSKLTVDKSRW 300  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 CompuGen Ltd.

protein - protein search, using sw model

on: October 27, 2004, 16:51:34 ; Search time 32.8826 Seconds  
(without alignments)  
665.548 Million cell updates/sec

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total number of hits satisfying chosen parameters: 478139

nimum DB seq length: 0  
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st-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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2: /cgn2\_6/ptodata/1/iaa/5B\_COMB.pep.\*  
3: /cgn2\_6/ptodata/1/iaa/6A\_COMB.pep.\*  
4: /cgn2\_6/ptodata/1/iaa/6B\_COMB.pep.\*  
5: /cgn2\_6/ptodata/1/iaa/PTUS\_COMB.pep.\*  
6: /cgn2\_6/ptodata/1/iaa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1729	98.0	371	1	US-08-236-311-7
2	1729	98.0	371	3	US-08-457-918-7
3	1729	98.0	371	4	US-10-157-408-7
4	1729	98.0	446	3	US-08-397-411-7
5	1729	98.0	449	1	US-08-458-516-13
6	1729	98.0	467	4	US-08-030-175-41
7	1729	98.0	467	4	US-08-030-175-42
8	1729	98.0	476	2	US-08-378-939-10
9	1729	98.0	547	4	US-09-746-359A-54
10	1729	98.0	567	4	US-09-825-561A-16
11	1729	98.0	571	4	US-09-746-359A-53
12	1729	98.0	951	4	US-09-313-942-9
13	1725	97.8	462	4	US-09-289-942A-7
14	1725	97.8	475	4	US-09-740-002-27
15	1725	97.8	476	3	US-08-487-550-4
16	1725	97.8	476	3	US-08-487-550-12
17	1725	97.8	476	4	US-09-526-098-4
18	1725	97.8	476	4	US-09-526-098-12
19	1725	97.8	476	4	US-09-383-916-4
20	1725	97.8	476	4	US-09-383-916-12
21	1725	97.8	478	4	US-08-487-550-8
22	1725	97.8	478	4	US-09-526-098-8
23	1725	97.8	478	4	US-09-383-916-8
24	1724	97.7	459	1	US-08-157-101A-7
25	1724	97.7	475	4	US-09-740-002-25
26	1723	97.7	330	4	US-09-301-593-22
27	1723	97.7	451	2	US-08-887-352B-14

28 1723 97.7 451 2 US-08-887-352B-16 Sequence 16, Appl  
29 1723 97.7 451 2 US-08-887-352B-18 Sequence 18, Appl  
30 1723 97.7 451 3 US-08-466-151-65 Sequence 65, Appl  
31 1723 97.7 451 3 US-09-109-207C-14 Sequence 14, Appl  
32 1723 97.7 451 3 US-09-109-207C-16 Sequence 16, Appl  
33 1723 97.7 451 3 US-09-109-207C-18 Sequence 18, Appl  
34 1723 97.7 451 3 US-09-282-505-2 Sequence 2, Appl  
35 1723 97.7 451 3 US-09-054-253-2 Sequence 2, Appl  
36 1723 97.7 451 3 US-09-296-005-14 Sequence 14, Appl  
37 1723 97.7 451 3 US-09-296-005-16 Sequence 16, Appl  
38 1723 97.7 451 3 US-09-296-005-18 Sequence 18, Appl  
39 1723 97.7 451 4 US-09-282-846-2 Sequence 2, Appl  
40 1723 97.7 451 4 US-09-680-145-2 Sequence 2, Appl  
41 1723 97.7 451 4 US-09-920-171-14 Sequence 14, Appl  
42 1723 97.7 451 4 US-09-920-171-16 Sequence 16, Appl  
43 1723 97.7 451 4 US-09-920-171-18 Sequence 18, Appl  
44 1723 97.7 451 4 US-09-716-028-14 Sequence 14, Appl  
45 1723 97.7 451 4 US-09-716-028-16 Sequence 16, Appl

ALIGNMENTS

RESULT 1  
US-08-236-311-7  
; Sequence 7, Application US/08236311  
; Patent No. 5565335  
; GENERAL INFORMATION:  
; APPLICANT: Capon, Daniel J.  
; APPLICANT: Gregory, Timothy J.  
; TITLE OF INVENTION: Adheson Variants  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: Genentech, Inc.  
; STREET: 460 Point San Bruno Blvd  
; CITY: South San Francisco  
; STATE: California  
; COUNTRY: USA  
; ZIP: 94080  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: 5 25 inch, 360 Kb floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: patin (Genentech)  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/236,311  
; FILING DATE: 02-MAY-1994  
; CLASSIFICATION: 435  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/936190  
; FILING DATE: 26-AUG-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/842777  
; FILING DATE: 18-FEB-1992  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/250785  
; FILING DATE: 28-SEP-1988  
; PRIOR APPLICATION DATA:  
; APPLICATION NUMBER: 07/104329  
; FILING DATE: 02-OCT-1987  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Hasak, Janet E.  
; REGISTRATION NUMBER: 28,616  
; REFERENCE/POCKET NUMBER: 444PIC2  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 415/225-1896  
; TELEFAX: 415/952-9881  
; TELEX: 910/371-7168  
; INFORMATION FOR SEQ ID NO: 7:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 371 amino acids  
; TYPE: amino acid  
; TOPOLOGY: linear

US-08-236-311-7

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Query Match          98.0%; Score 1729; DB 1; Length 371;
Best Local Similarity 97.9%; Pred. No. 3e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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QY 61 GLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPELLGG 120
DB 102 GLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPELLGG 161
QY 121 PSVLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180
DB 162 PSVLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 221
QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 222 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 281
QY 241 LTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDVSGSFYFLYSLKLTVDKSRW 300
DB 282 LTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDVSGSFYFLYSLKLTVDKSRW 341
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 342 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 371

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## RESULT 2

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US-08-457-918-7
; Sequence 7, Application US/08457918
; Patent No. 6117655
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/936190
; FILING DATE: 26-AUG-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/842777
; FILING DATE: 18-FEB-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/250785
; FILING DATE: 28-SEP-1988
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 07/104329
; FILING DATE: 02-OCT-1987
; ATTORNEY/AGENT INFORMATION:
; NAME: Kubinec, Jeffrey S.

```

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; REGISTRATION NUMBER: 36,575
; REFERENCE/DOCKET NUMBER: P0444PLC3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-8228
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 371 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
US-08-457-918-7

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Query Match 98.0%; Score 1729; DB 3; Length 371;

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Best Local Similarity 97.9%; Pred. No. 3e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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DB 42 ASTKGPSVFPLAPSSKSTSGTAAAGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 101
QY 61 GLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPELLGG 120
DB 102 GLYSLSSVTVVPSSSLGTQTYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPELLGG 161
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DB 162 PSVLFPPPKDPTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 221
QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 222 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 281
QY 241 LTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDVSGSFYFLYSLKLTVDKSRW 300
DB 282 LTKNQVSLTCLVKGYFSPDIAVEWESNGQPENNYKTTTPVLDVSGSFYFLYSLKLTVDKSRW 341
QY 301 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 330
DB 342 QQGNVFSCVMHEALHNHYTQKSLSLSPGK 371

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## RESULT 3

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US-10-157-408-7
; Sequence 7, Application US/10157408
; Patent No. 6710169
; GENERAL INFORMATION:
; APPLICANT: Capon, Daniel J.
; APPLICANT: Gregory, Timothy J.
; TITLE OF INVENTION: Adhesion Variants
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: patin (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/157,408
; FILING DATE: 28-May-2002
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/457,918
; FILING DATE: 1-JUN-1995
; APPLICATION NUMBER: 08/236311
; FILING DATE: 02-MAY-1994
; APPLICATION NUMBER: 07/936190

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FILING DATE: 26-AUG-1992  
 APPLICATION NUMBER: 07/842777  
 FILING DATE: 18-FEB-1992  
 APPLICATION NUMBER: 07/250785  
 FILING DATE: 28-SEP-1988  
 APPLICATION NUMBER: 07/104329  
 FILING DATE: 02-OCT-1987  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Kubinec, Jeffrey S.  
 REGISTRATION NUMBER: 36,575  
 REFERENCE/DOCKET NUMBER: P0444P1C3  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415/225-8228  
 TELEFAX: 415/952-9881  
 TELEX: 910/371-7168  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 371 amino acids  
 TYPE: amino acid  
 TOPOLOGY: linear  
 SEQUENCE DESCRIPTION: SEQ ID NO: 7:  
 1-10-157-408-7

Query Match 98.0%; Score 1729; DB 4; Length 371;  
 Best Local Similarity 97.9%; Pred. No. 3e-157;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
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 61 GLYSLSSVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPPEAPLGG 120  
 102 GLYSLSSVTVFPSSSLGTQTYICNVNHPKSNKVDKVEPKSCDKHTHTCPPEAPLGG 161  
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 181 STYRVSVTLVTHQNMWNGKEYCKKVSNNKALPAIEKTIKAKVQPREPOVYTLPPSRDE 240  
 222 STYRVSVTLVTHQNMWNGKEYCKKVSNNKALPAIEKTIKAKVQPREPOVYTLPPSRDE 281  
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RESULT 4  
 3-08-397-411-7  
 Sequence 7, Application US/08397411  
 Patent No. 6129914  
 GENERAL INFORMATION:  
 APPLICANT: Weiner, George  
 APPLICANT: Gingrich, Roger  
 APPLICANT: Link, Brian  
 APPLICANT: Tso, J. Yun  
 TITLE OF INVENTION: Bispecific Antibody Effective to Treat  
 TITLE OF INVENTION: B-Cell Lymphoma and Cell Line  
 NUMBER OF SEQUENCES: 14  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: Townsend and Townsend and Crew  
 STREET: One Market Plaza, Steuart Tower, Suite 2000  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94105  
 COMPUTER READABLE FORM:  
 MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible  
 OPERATING SYSTEM: PC-DOS/MS-DOS  
 SOFTWARE: PatentIn Release #1.0, Version #1.25  
 CURRENT APPLICATION DATA: US/08/397,411  
 APPLICATION NUMBER: 07/250785  
 FILING DATE: 28-SEP-1988  
 APPLICATION NUMBER: 07/104329  
 FILING DATE: 02-OCT-1987  
 PRIOR APPLICATION DATA:  
 APPLICATION NUMBER: US 07/859,583  
 FILING DATE: 27-MAR-1992  
 ATTORNEY/AGENT INFORMATION:  
 NAME: Smith, William M.  
 REGISTRATION NUMBER: 30,223  
 REFERENCE/DOCKET NUMBER: 011823-004901  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: 415-326-2400  
 TELEFAX: 415-326-2422  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 446 amino acids  
 TYPE: amino acid  
 STRANDEDNESS: single  
 TOPOLOGY: linear  
 MOLECULE TYPE: peptide  
 US-08-397-411-7

Query Match 98.0%; Score 1729; DB 3; Length 446;  
 Best Local Similarity 97.9%; Pred. No. 3.9e-157;  
 Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
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 181 STYRVSVTLVTHQNMWNGKEYCKKVSNNKALPAIEKTIKAKVQPREPOVYTLPPSRDE 240  
 297 STYRVSVTLVTHQNMWNGKEYCKKVSNNKALPAIEKTIKAKVQPREPOVYTLPPSRDE 356  
 241 LTKQVSLTCLVKGFPSPDIKAVESNGQPNENYKTPPVLDVSGSFLLYKLTVDKSRW 300  
 357 LTKQVSLTCLVKGFPSPDIKAVESNGQPNENYKTPPVLDVSGSFLLYKLTVDKSRW 416  
 301 QQGNVFCSCVMHEALHNHYQORSLSLSPGK 330  
 417 QQGNVFCSCVMHEALHNHYQORSLSLSPGK 446

RESULT 5  
 US-08-458-516-13  
 Sequence 13, Application US/08458516  
 Patent No. 577085  
 GENERAL INFORMATION:  
 APPLICANT: Co, Man Surg  
 APPLICANT: Tso, J. Yun  
 TITLE OF INVENTION: Humanized Antibodies Reactive with  
 TITLE OF INVENTION: GPIIB/IIIA  
 NUMBER OF SEQUENCES: 23  
 CORRESPONDENCE ADDRESS:  
 ADDRESSEE: William M. Smith  
 STREET: One Market Plaza, Steuart Tower, Suite 2000  
 CITY: San Francisco  
 STATE: California  
 COUNTRY: USA  
 ZIP: 94105  
 COMPUTER READABLE FORM:

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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-458-516-13

Query Match 98.0%; Score 1729; DB 1; Length 449;
Best Local Similarity 97.9%; Pred. No. 4e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGSPVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 120 ASTKGSPVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179
QY 61 GLYSLSSVTVFPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELLGG 120
DB 180 GLYSLSSVTVFPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELLGG 239
QY 121 PSVELFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 180
DB 240 PSVELFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 299
QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 300 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 359
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 300
DB 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 419
QY 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
DB 420 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 449

RESULT 6
US-030-175-41
; Sequence 41, Application US/08030175
; Patent No. 6767996
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D.
; APPLICANT: Clark, Michael R.
; APPLICANT: Cobbold, Stephen P.
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
; STREET: 555 13TH ST., NW Suite 701 East
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/458,516
; FILING DATE:
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/059,159
; FILING DATE: 03-MAY-1993
; ATTORNEY/AGENT INFORMATION:
; NAME: Smith, William M.
; REGISTRATION NUMBER: 30,223
; REFERENCE/DOCKET NUMBER: 11823-37-3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-326-2400
; TELEFAX: 415-326-2422
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 449 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-458-516-13

Query Match 98.0%; Score 1729; DB 1; Length 449;
Best Local Similarity 97.9%; Pred. No. 4e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGSPVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60
DB 120 ASTKGSPVFPLAPSKSTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 179
QY 61 GLYSLSSVTVFPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELLGG 120
DB 180 GLYSLSSVTVFPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPELLGG 239
QY 121 PSVELFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 180
DB 240 PSVELFPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYDGVGVHVNKTKPREQYN 299
QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
DB 300 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 359
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 300
DB 360 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTPVLDVSGSFYLYSKLTVDKSRW 419
QY 301 QQGNVFSCSVMEALHNHYQOQSLSLSPGK 330
DB 420 QQGNVFSCSVMEALHNHYTQKSLSLSPGK 449

RESULT 7
US-030-175-42
; Sequence 42, Application US/08030175
; Patent No. 6767996
; GENERAL INFORMATION:
; APPLICANT: Gorman, Scott D.
; APPLICANT: Clark, Michael R.
; APPLICANT: Cobbold, Stephen P.
; APPLICANT: Waldmann, Herman
; TITLE OF INVENTION: ALTERED ANTIBODIES AND THEIR PREPARATION
; NUMBER OF SEQUENCES: 43
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Rothwell, Figg, Ernst & Kurz, P. C.
; STREET: 555 13TH ST., NW Suite 701 East
; CITY: Washington
; STATE: D. C.
; COUNTRY: U.S.
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COUNTRY: U.S.  
ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM AT compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS V 3.2  
SOFTWARE: Wordperfect 5.0 (Dos Text)  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/030,175  
FILING DATE: 17-MAY-1993  
CLASSIFICATION: 424  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: PCT/GB91/01578  
FILING DATE: 13-SEP-1991  
ATTORNEY/AGENT INFORMATION:  
NAME: Ernst, Barbara G.  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1768-113  
TELEPHONE: (202)783-6040  
TELEFAX: (202)783-6031  
INFORMATION FOR SEQ ID NO: 42:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 467 amino acids  
/ TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-030-175-42

Query Match 98.0%; Score 1729; DB 4; Length 467;  
Best Local Similarity 97.9%; Pred. No. 4.2e-157;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYRPEPTVSVWNSGALTSGVHTFPAVLQSS 60  
138 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYRPEPTVSVWNSGALTSGVHTFPAVLQSS 197  
61 GLYSLSSVTVVPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120  
198 GLYSLSSVTVVPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 257  
121 PSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQYN 180  
258 PSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQYN 317  
181 STYRVSVLTVLHQNWNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240  
318 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 377  
241 LTKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGVSGFFLYSKLTVDKSRW 300  
378 LTKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGVSGFFLYSKLTVDKSRW 437  
301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330  
438 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 467

RESULT 8  
US-08-378-939-10  
Sequence 10, Application US/08378939  
Patent No. 5876961  
GENERAL INFORMATION:  
APPLICANT: CROWE, JAMES SCOTT  
APPLICANT: LEWIS, ALAN PETER  
TITLE OF INVENTION: PRODUCTION OF ANTIBODIES  
NUMBER OF SEQUENCES: 46  
CORRESPONDENCE ADDRESS:  
ADDRESSER: ROTHWELL, FIGG, ERNST & KURZ  
STREET: 555 THIRTEENTH ST. N.W.  
CITY: WASHINGTON  
STATE: D.C.  
COUNTRY: U.S.

ZIP: 20004  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: Patent In Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/378,939  
FILING DATE:  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/952640  
FILING DATE: 01-DEC-1992  
ATTORNEY/AGENT INFORMATION:  
NAME: ERNST, BARBARA G.  
REGISTRATION NUMBER: 30,377  
REFERENCE/DOCKET NUMBER: 1808-118  
TELEPHONE: (202) 783-6040  
TELEFAX: (202) 783-6031  
INFORMATION FOR SEQ ID NO: 10:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 476 amino acids  
/ TYPE: amino acid  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-378-939-10

Query Match 98.0%; Score 1729; DB 2; Length 476;  
Best Local Similarity 97.9%; Pred. No. 4.3e-157;  
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYRPEPTVSVWNSGALTSGVHTFPAVLQSS 60  
DB 147 ASTKGPSVFPLAPSSKSTSGTAAALGCLVKDYRPEPTVSVWNSGALTSGVHTFPAVLQSS 206  
QY 61 GLYSLSSVTVVPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120  
DB 207 GLYSLSSVTVVPSSSLGTQYICNVNHPKNTKVDKVEPKSCDKTHTCPPCPAPPELLGG 266  
QY 121 PSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQYN 180  
DB 267 PSVFLFPPKPKDLMISRTPEVTCVVDVSHEDPEVKFNMYVDGVEVHNKTKPREEQYN 326  
QY 181 STYRVSVLTVLHQNWNGKEYKCKVSNKALPAPIEKTISKAKVQPREPOVYTLPPSRDE 240  
DB 327 STYRVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKTISKAKGQPREPOVYTLPPSRDE 386  
QY 241 LTKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGVSGFFLYSKLTVDKSRW 300  
DB 387 LTKQVSLTCLVKGFPYSDIAVEWESNGQPENNYKTPPVLDSDGVSGFFLYSKLTVDKSRW 446  
QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330  
DB 447 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 476

RESULT 9  
US-09-746-359A-54  
Sequence 54, Application US/09746359A  
Patent No. 6610286  
GENERAL INFORMATION:  
APPLICANT: Thompson, Penny  
APPLICANT: Foster, Donald C.  
APPLICANT: Xu, Wenfeng  
APPLICANT: Madden, Karen L.  
APPLICANT: Kelly, James D.  
APPLICANT: Sprecher, Cindy A.  
APPLICANT: Blumberg, Hal  
APPLICANT: Eagan, Maribeth A.  
APPLICANT: Jaspers, Stephen R.  
APPLICANT: Chandrasekhar, Yamin A.  
APPLICANT: No. 6610286ak, Julia E.

```
; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21, 969
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 54
; LENGTH: 547
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-54

Query Match      98.0%; Score 1729; DB 4; Length 547;
Best Local Similarity 97.9%; Pred. No. 5.3e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 218 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 277
QY 61 GLYSLSVVTVFPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Db 278 GLYSLSVVTVFPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 337
QY 121 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNHNTKPREEQYN 180
Db 338 PSVFLFPPPKDPTLMISRTPEVTCVVVDVSHEDPEVKFNWYDGVGVHNHNTKPREEQYN 397
QY 181 STYRWSVLTVLHQNWNHNGEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240
Db 398 STYRWSVLTVLHQNWNHNGEYKCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 457
QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 300
Db 458 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGVFFLYSKLTVDKSRW 517
QY 301 QQGNVFCSVMHEALHNHYQOQSLSLSPGK 330
Db 518 QQGNVFCSVMHEALHNHYQOQSLSLSPGK 547

RESULT 10
US-09-825-561A-16
; Sequence 16, Application US/09825561A
; Patent No. 6777539
; GENERAL INFORMATION:
; APPLICANT: Sprecher, Cindy A.
; APPLICANT: No. 6777539ak, Julia E.
; APPLICANT: West, James W.
; APPLICANT: Presnell, Scott R.
; APPLICANT: Holly, Richard D.
; APPLICANT: Nelson, Andrew J.
; TITLE OF INVENTION: SOLUBLE ZALPHA11 CYTOKINE RECEPTORS
; FILE REFERENCE: 00-22
; CURRENT APPLICATION NUMBER: US/09/825,561A
; CURRENT FILING DATE: 2000-04-05
; PRIOR FILING DATE: 2000-04-05
; PRIOR APPLICATION NUMBER: US 60/222,121
; PRIOR FILING DATE: 2000-07-28
; NUMBER OF SEQ ID NOS: 86
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 16
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: soluble zalpha11/IgGammal polypeptide
US-09-825-561A-16

Query Match      98.0%; Score 1729; DB 4; Length 571;
Best Local Similarity 97.9%; Pred. No. 5.7e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 242 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 301
QY 61 GLYSLSVVTVFPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Db 302 GLYSLSVVTVFPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 361

; TITLE OF INVENTION: Method for Treating Inflammation
; FILE REFERENCE: 99-108
; CURRENT APPLICATION NUMBER: US/09/746,359A
; CURRENT FILING DATE: 2001-05-21
; PRIOR APPLICATION NUMBER: 60/171,969
; PRIOR FILING DATE: 1999-12-23
; PRIOR APPLICATION NUMBER: 60/213,341
; PRIOR FILING DATE: 2000-06-22
; NUMBER OF SEQ ID NOS: 72
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 53
; LENGTH: 571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-746-359A-53

Query Match      98.0%; Score 1729; DB 4; Length 571;
Best Local Similarity 97.9%; Pred. No. 5.7e-157;
Matches 323; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 60
Db 242 ASTKGPSVFPPLAPSSKSTSGGTAALGCLVKDYFPEPVTVSWNSGALTSGVHTFPAVLQSS 301
QY 61 GLYSLSVVTVFPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 120
Db 302 GLYSLSVVTVFPSSSLGTQYICNVNHPKSNKVDKVEPKSCDKTHTCCPCPAPELLGG 361
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Query Match 97.8%; Score 1725; DB 4; Length 475;  
 Best Local Similarity 97.6%; Pred. No. 1e-156;  
 Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 DB 146 ASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 205

QY 61 GLYSLSSVTVFPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120  
 DB 206 GLYSLSSVTVFPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELLGG 265

QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
 DB 266 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 325

QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 DB 326 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 385

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFFLYSKLTVDKSRW 300  
 DB 386 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFFLYSKLTVDKSRW 445

QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330  
 DB 446 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 475

RESULT 15  
 US-08-487-550-4  
 ; Sequence 4, Application US/08487550  
 ; Patent No. 6113898  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Anderson, Darrell R.  
 ; TITLE OF INVENTION: "MONKEY MONOCLONAL ANTIBODIES SPECIFIC  
 ; TITLE OF INVENTION: TO HUMAN B7.1 AND/OR B7.2 PRIMATIZED FORMS THEREOF,  
 ; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING, AND USE THEREOF AS  
 ; TITLE OF INVENTION: IMMUNOSUPPRESSANTS"  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BURNS, DOANE, SWECKER & MATHIS  
 ; STREET: 699 Prince Street  
 ; CITY: Alexandria  
 ; STATE: VA  
 ; COUNTRY: USA  
 ; ZIP: 22314  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patent in Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/487,550  
 ; FILING DATE: 07-JUN-1995  
 ; CLASSIFICATION: 435  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Teskin, Robin L.  
 ; REGISTRATION NUMBER: 35,030  
 ; REFERENCE/DOCKET NUMBER: 012712-131  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 703-836-6620  
 ; TELEFAX: 703-836-2021  
 ; INFORMATION FOR SEQ ID NO: 4:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 476 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 US-08-487-550-4

Query Match 97.8%; Score 1725; DB 3; Length 476;  
 Best Local Similarity 97.6%; Pred. No. 1e-156;

Matches 322; Conservative 3; Mismatches 5; Indels 0; Gaps 0;

QY 1 ASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 60  
 DB 147 ASTKGPSVFPPLAPSSKTSGGTAALGCLVKDYFPEPTVSWNSGALTSGVHTFPAVLQSS 206

QY 61 GLYSLSSVTVFPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELLGG 120  
 DB 207 GLYSLSSVTVFPSSSLGTQYICNVNHPKSNKTKVDKVEPKSCDKTHTCPPCPAPPELLGG 266

QY 121 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 180  
 DB 267 PSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKFNWYVDGVEVHNKTKPREEQYN 326

QY 181 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 240  
 DB 327 STYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKTISKAKVQPREPQVYTLPPSRDE 386

QY 241 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFFLYSKLTVDKSRW 300  
 DB 387 LTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTPPVLDVSGSFFLYSKLTVDKSRW 446

QY 301 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 330  
 DB 447 QQGNVFCSCVMHEALHNHYQOQSLSLSPGK 476

Search completed: October 27, 2004, 17:05:52  
 Job time : 34.8826 secs

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4 protein - protein search, using sw model

run on: October 27, 2004, 16:51:09 / Search time 20.2278 Seconds  
(without alignments)  
1103.547 Million cell updates/sec

title: US-10-000-439-3

affect score: 1260  
sequence: 1 EPKSCDTHPCPCAPPELL.....MHEALNHVQORSLSPQK 232

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

sarched: 283416 seqs, 96216763 residues

otal number of hits satisfying chosen parameters: 283416

inimum DB seq length: 0

aximum DB seq length: 2000000000

st-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

itabase :

PIR\_79:\*  
1: PIR1.\*  
2: PIR2.\*  
3: PIR3.\*  
4: PIR4.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	330	1 GHU	IG gamma-1 chain C
2	1219	96.7	374	2 S69339	IG heavy chain V x
3	1217	96.6	255	4 S31866	IG gamma-1 chain C
4	1172	93.0	234	2 P70207	IG gamma chain C r
5	1138	90.3	377	2 A23511	IG gamma-3 chain C
6	1136	90.2	377	2 A60764	IG gamma-3 chain C
7	1123	89.1	289	1 G3HUWI	IG gamma-3 heavy C
8	1107	87.9	326	1 G2HU	IG gamma-2 chain C
9	1097	87.1	327	1 G4HU	IG gamma-4 chain C
10	883	70.1	323	1 GHRB	IG gamma chain C r
11	868.5	68.9	328	2 I47160	IG gamma 2b chain
12	868.5	68.9	328	2 I47159	IG gamma 2a chain
13	865	68.7	277	2 I47162	IG gamma 4 chain C
14	858	68.1	329	1 G2GP	IG gamma-2 chain C
15	847.5	67.3	328	2 I47158	IG gamma 1 chain c
16	840.5	66.7	328	2 I47161	IG gamma 3 chain c
17	820	65.1	470	2 S2080	IG heavy chain pre
18	813	64.5	333	2 P60018	IG gamma-2b chain C
19	812.5	64.5	329	1 G2MSC	IG gamma-3 chain C
20	811.5	64.4	308	2 C30554	IG heavy chain C r
21	811.5	64.4	372	2 S31459	IG gamma-1 chain -
22	801.5	63.6	398	1 G3GSM	IG gamma-3 chain C
23	794.5	63.1	444	2 PC4436	monoclonal antibody
24	789.5	62.7	324	1 G3MS	IG gamma-1 chain C
25	784.5	62.3	326	2 G50017	IG gamma-1 chain C
26	784.5	62.3	393	1 G3MSM	IG gamma-1 chain C
27	776.5	61.6	329	2 S00847	IG gamma-2c chain
28	776	61.6	330	1 G2MSA	IG gamma-2a chain
29	776	61.6	469	2 S37483	IG gamma-2a chain

30 772 61.3 335 1 G2MSAB  
31 771 61.2 399 1 G2MSAM  
32 761 60.4 446 2 S40295  
33 751.5 59.6 474 1 G2MS11  
34 747.5 59.3 322 2 P80019  
35 746.5 59.2 405 1 G2MSBM  
36 735 58.3 327 2 S06611  
37 731.5 58.1 475 2 S01321  
38 669 53.1 180 2 I46732  
39 549 43.6 249 2 S69340  
40 547 43.4 218 2 A36040  
41 542 43.0 152 2 S14236  
42 366.5 29.1 572 2 B46529  
43 357 28.3 549 2 S04845  
44 353 28.0 343 2 S25644  
45 353 28.0 455 1 MHMS

IG gamma-2a chain  
IG gamma-2a chain  
IG gamma-2a chain  
IG gamma-2a chain  
IG gamma-2a chain  
IG gamma-2 chain C  
IG gamma-2b chain  
IG gamma heavy cha  
IG heavy chain VHI  
IG heavy chain V-I  
IG gamma-1 chain C  
IG Y heavy chain (  
IG heavy chain pre  
IG mu chain C regi  
IG mu chain C regi

## ALIGNMENTS

### RESULT 1

GHU

IG gamma-1 chain C region - human

C/Species: Homo sapiens (man)

C/Date: 31-Jan-1981 #sequence revision 18-Aug-1982 #text change 09-Jul-2004

C/Accession: A93433; S36861; S33887; B90563; A90564; B91668; A91723; A02146

R/Fellison, J.W.; Berson, E.U.; Hood, L.E.

Nucleic Acids Res. 10, 4071-4079, 1982

A/Title: The nucleotide sequence of a human immunoglobulin C-gamma1 gene.

A/Reference number: A93433; MUID:82274238; PMID:6287432

A/Accession: A93433

A/Molecule type: DNA

A/Residues: 1-330 <ELL>

A/Cross-references: UNIPROT:P01857; EMBL:Z17370

A/Note: this sequence has the G1m(17) allotypic marker, 97-Lys, and the G1m(1) markers, 2

A/Note: Lys-330 is removed after translation

R/Harris, L.J.

submitted to the EMBL Data Library, October 1992

A/Reference number: S33904

A/Accession: S36861

A/Molecule type: DNA

A/Residues: 2-330 <HAR>

A/Cross-references: EMBL:Z17370

R/Takahashi, N.; Ueda, S.; Obata, M.; Nikaido, T.; Nakai, S.; Honjo, T.

Cell 29, 671-679, 1982

A/Title: Structure of human immunoglobulin gamma genes: implications for evolution of a s

A/Reference number: S33887; MUID:83001943; PMID:6811139

A/Accession: S33887

A/Molecule type: DNA

A/Residues: 88-113/235-330 <TAK>

R/Cunningham, B.A.; Rutishauser, U.; Gall, W.E.; Gottlieb, P.D.; Waxdal, M.J.; Edelman, C

Biochemistry 9, 3161-3170, 1970

A/Title: The covalent structure of a human gammaG-immunoglobulin. VII. Amino acid sequenc

A/Reference number: A90563; MUID:71064024; PMID:5489771

A/Contents: myeloma protein Eu

A/Accession: B90563

A/Molecule type: protein

A/Residues: 1-96, 'R', 98-135 <CUN>

A/Note: this sequence has the G1m(3) marker, 97-Arg

R/Rutishauser, U.; Cunningham, B.A.; Bennett, C.; Konigsberg, W.H.; Edelman, G.M.

Biochemistry 9, 3171-3181, 1970

A/Title: The covalent structure of a human gammaG-immunoglobulin. VIII. Amino acid sequer

A/Reference number: A90564; MUID:71064025; PMID:5530842

A/Contents: Eu

A/Accession: A90564

A/Molecule type: protein

A/Residues: 136-154, 'Q', 156-165, 'Q', 167-176, 'Q', 178-194, 'N', 196-197, 'D', 199-238, 'E', 240, 'E'

A/Note: this sequence has the G1m(non-1) markers, 239-Glu and 241-Met

R/Ponstingl, H.; Hilschmann, N.

Hoppe-Seyler's Z. Physiol. Chem. 357, 1571-1604, 1976

A/Title: Die Primerstruktur eines monoklonalen IgG1-Immunglobulins (Myelomprotein Nie),

## igen Primaerstruktur.

A:Reference number: A91668; MUID:77070269; PMID:826475  
A:Contents: myeloma protein Nie  
A:Accession: B91668  
A:Molecule type: protein  
A:Residues: 1-34, 'Q', 36-96, 'K', 98-115, 'O', 117-197, 'D', 199-238, 'D', 240, 'L', 242-268, 'E', 27  
A>Note: this sequence has the Gln(17) and Gln(11) markers  
R:Schmidt, W.E.; Jung, H.D.; Palm, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 364, 713-747, 1983  
A:Title: Die Primaerstruktur des kristallisierten monoklonalen Immunglobulins IgG1 KO  
A:Reference number: A91723; MUID:83289131; PMID:6884994  
A:Contents: myeloma protein KOB; disulfide bonds  
A:Accession: A91723  
A:Molecule type: protein  
A:Residues: 1-96, 'R', 98-197, 'D', 199-238, 'E', 240, 'M', 242-266, 'D', 268-271, 'D', 273-330 <SCH  
A>Note: this sequence has the Gln(3) and Gln(non-1) markers  
R:Gall, W.E.; Edelman, G.M.  
Biochemistry 9, 3188-3196, 1970  
A:Title: The covalent structure of a human gammaG-immunoglobulin. X. Intrachain disulfid  
A:Reference number: A90565; MUID:71064027; PMID:4923144  
A:Contents: annotation; disulfide bonds  
R:Dreker, L.; Schwarz, J.; Reichel, W.; Hilschmann, N.  
Hoppe-Seyler's Z. Physiol. Chem. 357, 1515-1540, 1976  
A:Title: Rule of antibody structure. The primary structure of monoclonal IgG1 immunoglob  
enamide cleavage products, and the disulfide bridges.  
A:Reference number: A91667; MUID:77070267; PMID:1002129  
A:Contents: annotation; disulfide bonds  
C:Genetics:  
A:Gene: GDB:IGHG1  
A:Cross-references: GDB:120085; OMIM:147100  
A:Map position: 14q32.33-14q32.33  
A:Introns: 99/1, 114/1, 224/1  
A:Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
hain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into 1a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
C:Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F:20-85/Domain: immunoglobulin homology <IMI>  
F:137-206/Domain: immunoglobulin homology <IM2>  
F:243-310/Domain: immunoglobulin homology <IM3>  
F:27-83, 144-204, 250-308/Disulfide bonds: #status experimental  
F:103/Disulfide bonds: interchain (to light chain) #status experimental  
F:103, 112/Disulfide bonds: interchain (to heavy chain) #status experimental  
F:180/Banding site: carbohydrate (Asn) (covalent) #status experimental  
Query Match 97.2%; Score 1225; DB 1; Length 330;  
Best Local Similarity 97.0%; Pred. No. 3.5e-85;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
Qy 1 EPKSCDKTHCPCPAPELLGGPSVFLPFPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
Db 99 EPKSCDKTHCPCPAPELLGGPSVFLPFPKDTLMISRTPEVTCVVDVSHEDPEVKF 158  
Qy 61 NWYVDGVEVHNKTPREEQYNSTYRVSVLTQLVKGFPSPDIQVNSKALPAPIEKT 120  
Db 159 NWYVDGVEVHNKTPREEQYNSTYRVSVLTQLVKGFPSPDIQVNSKALPAPIEKT 218  
Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
Db 219 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 278  
Qy 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQKRSLSLSPGK 232  
Db 279 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQKRSLSLSPGK 330  
RESULT 2  
S69339  
Ig heavy chain V region precursor - human  
C:Species: Homo sapiens (man)  
C:Date: 19-Mar-1997 #sequence\_revision 19-Mar-1997 #text\_change 01-Dec-2000  
A:Accession: S69339; S72664  
R:Khamilichi, A.A.; Aucouturier, P.; Preud'homme, J.L.; Cogne, M.  
Eur. J. Biochem. 229, 54-60, 1995

A:Title: Structure of abnormal heavy chains in human heavy-chain-deposition disease.  
A:Reference number: S69339; MUID:95262687; PMID:7744049

A:Accession: S69339  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-374 <KHA>  
A:Cross-references: EMBL:X81695  
R:Khamilichi, A.A.  
submitted to the EMBL Data Library, September 1994

A:Reference number: S72664  
A:Accession: S72664  
A:Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-140, 'C', 142-374 <KH2>  
A:Cross-references: EMBL:X81695  
C:Superfamily: immunoglobulin C region; immunoglobulin homology

Query Match 96.7%; Score 1219; DB 2; Length 374;  
Best Local Similarity 96.1%; Pred. No. 1.2e-84;  
Matches 223; Conservative 5; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCPCPAPELLGGPSVFLPFPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

Db 143 EPKSCDKTHCPCPAPELLGGPSVFLPFPKDTLMISRTPEVTCVVDVSHEDPEVKF 202

Qy 61 NWYVDGVEVHNKTPREEQYNSTYRVSVLTQLVQNMNGKCYKCKVSNKALPAPIEKT 120

Db 203 NWYVDGVEVHNKTPREEQYNSTYRVSVLTQLVQNMNGKCYKCKVSNKALPAPIEKT 262

Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180

Db 263 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 322

Qy 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQKRSLSLSPGK 232

Db 323 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQKRSLSLSPGK 374

## RESULT 3

S31866

Ig gamma-1 chain C region - synthetic

C:Species: synthetic

A:Note: Homo sapiens (man) gene engineered and expressed in Escherichia coli

C:Date: 06-Jan-1995 #sequence\_revision 17-Mar-1997 #text\_change 19-May-2000

C:Accession: S31866

R:Filpula, D.

submitted to the EMBL Data Library, February 1993

A:Description: Screening method for protein-protein interactions of cloned gene products

A:Reference number: S31866

A:Accession: S31866

A:Molecule type: mRNA

A:Residues: 1-255 <FIL>

A:Cross-references: EMBL:X70421; NID:G33068; PIDN:CAA49866.1; PID:G33069

C:Keywords: immunoglobulin

F:1-22/Region: Escherichia coli outer membrane protein A precursor

F:23-255/Region: human Ig gamma-1 chain C region

Query Match 96.6%; Score 1217; DB 4; Length 255;

Best Local Similarity 96.6%; Pred. No. 1e-84; 5; Indels 0; Gaps 0;

Matches 224; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHCPCPAPELLGGPSVFLPFPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

Db 24 ESXSCDKTHCPCPAPELLGGPSVFLPFPKDTLMISRTPEVTCVVDVSHEDPEVKF 83

Qy 61 NWYVDGVEVHNKTPREEQYNSTYRVSVLTQLVQNMNGKCYKCKVSNKALPAPIEKT 120

Db 84 NWYVDGVEVHNKTPREEQYNSTYRVSVLTQLVQNMNGKCYKCKVSNKALPAPIEKT 143

Qy 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180

Db 144 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 203



A;Title: Primary structure of the 'hinge' region of human IgG3. Probable quadruplication  
A;Reference number: A92219; MUID:77118561; PMID:402363  
A;Contents: normal gamma-3 chains, sequence corresponding to residues 12-97 of protein W  
A;Accession: A92219  
A;Molecule type: protein  
A;Residues: 12-97 <MIC>  
A;Note: The hinge region in gamma-3 chains is about four times as long as in other gamma  
chain segment (12-28)  
A;Note: cysteines at positions 24, 27, 33, 39, 42, 48, 54, 57, 63, 69, and 72 form inter  
B;Wolfenstein-Todell, C.; Frangione, B.; Prelli, F.; Franklin, E.C.  
Biochem. Biophys. Res. Commun. 71, 907-914, 1976  
A;Title: The amino acid sequence of 'heavy chain disease' protein ZUC. Structure of the  
A;Reference number: A90198; MUID:77021516; PMID:823945  
A;Contents: heavy chain disease protein Zuc, partial sequence corresponding to residues  
A;Accession: A90198  
A;Molecule type: protein  
A;Residues: 59-125, 'BB', 128-226, 228-289 <WOL>  
A;Note: This protein lacks most of the V region, all of the CH1 region, and part of the  
R;Alexander, A.; Steinmetz, M.; Barrault, D.; Frangione, B.; Franklin, E.C.; Hood, L.  
Proc. Natl. Acad. Sci. U.S.A. 79, 3260-3264, 1982  
A;Title: gamma heavy chain disease in man: cDNA sequence supports partial gene deletion  
A;Reference number: A93915; MUID:82247835; PMID:6908505  
A;Contents: heavy chain disease protein Omm  
A;Accession: A93915  
A;Molecule type: mRNA  
A;Residues: 12-70, 72-114, 116-125, 'E', 127-133, 'L', 135-136, 'E', 138, 'Y', 140-154, 'D', 156-157  
A;Note: a carboxyl-terminal Lys is removed posttranslationally  
A;Note: This sequence may represent an allelic form or another gamma chain subclass  
C;Comment: The heavy chain disease protein Wis is shown.  
C;Genetics:  
A;Gene: GDB:IGHG3  
A;Cross-references: GDB:119339; OMIM:147120  
A;Map position: 14q32.33-14q32.33  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; immunoglobulin; pyroglyutamic acid  
F;203-270/Domain: immunoglobulin homology <IMM>  
F;1/Modified site: pyroglutamate carboxylic acid (Gln) #status experimental  
F;6,140/Binding site: carbohydrate (Asn) (covalent) #status experimental

Query Match 89.1%; Score 1123; DB 1; Length 289;  
Best Local Similarity 88.3%; Pred. No. 1.5e-77;  
Matches 204; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

Qy 1 EPKCDKTHTCPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 59 EPKCDTPPCPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 118

Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWNGKYEYCKVSKNKPAPIEKT 120  
Db 119 KWIYVDGVQVHNKTKPREEQYNSTYRVVSVLTVLHQNWLDGKYEYCKVSKNKPAPIEKT 178

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEESGQPENNYKTP 180  
Db 179 ISKTKGQPREPQVYTLPPSRDEMKKNQVSLTCLVKGFYPSDIAVEESGQPENNYNTTP 238

Qy 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSNVHEALHNHYQQRSLSPG 231  
Db 239 PMLDSGDSGFFLYSKLTVDKSRWQGNVFCVSNVHEALHNRYTKSLSPG 289

RESULT 8  
GSHU  
Ig gamma-2 chain C region - human  
C;Species: Homo sapiens (man)  
C;Date: 30-Apr-1981 #sequence revision 13-Jun-1983 #text\_change 09-Jul-2004  
C;Accession: A93906; A92809; A90752; A93132; A02148  
R;Ellison, J.; Hood, L.; U.S.A. 79, 1984-1988, 1982  
Proc. Natl. Acad. Sci. U.S.A. 79, 1984-1988, 1982  
A;Title: Linkage and sequence homology of two human immunoglobulin gamma heavy chain con  
A;Reference number: A93906; MUID:82197621; PMID:6804948  
A;Accession: A93906  
A;Molecule type: DNA  
A;Residues: 1-326 <ELL>

A;Cross-references: UNIPROT:P01859; GB:V00554; GB:J00230; NID:932759; PIDN:CAB58438.1; I  
A;Note: Lys-326 is probably removed posttranslationally  
R;Wang, A.C.; Tung, E.; Fudenberg, H.H.  
J. Immunol. 125, 1048-1054, 1980  
A;Title: The primary structure of a human IgG2 heavy chain: genetic, evolutionary, and f  
A;Reference number: A92809; MUID:81007873; PMID:6774012  
A;Contents: myeloma protein TII  
A;Accession: A92809  
A;Molecule type: protein  
A;Residues: 1-19, 'Q', 21-57, 'Z', 59, 'A', 61-193, 'D', 195-325 <WAN>  
A;Note: Trp-156 is at or near the complement-binding site  
R;Connell, G.E.; Parr, D.M.; Hofmann, T.  
Can. J. Biochem. 57, 758-767, 1979  
A;Title: The amino acid sequences of the three heavy chain constant region domains of a  
A;Reference number: A90752; MUID:80001357; PMID:113060  
A;Contents: myeloma protein Zie  
A;Accession: A90752  
A;Molecule type: protein  
A;Residues: 1-24, 'E', 26-57, 'EV', 60-85, 132-171, 'ZZZ', 175, 'B', 177-193, 'D', 195-196, 'Q', 198-  
A;Note: this sequence has since been revised  
R;Hofmann, T.; Parr, D.M.  
Mol. Immunol. 16, 923-925, 1979  
A;Title: A note on the amino acid sequence of residues 381-391 of human immunoglobulin s  
A;Reference number: A93132; MUID:80114419; PMID:118920  
A;Contents: Zie  
A;Accession: A93132  
A;Molecule type: protein  
A;Residues: 238-275 <HOF>  
R;Hofmann, T.; Parr, D.M.  
submitted to the Atlas, March 1980  
A;Reference number: A94591  
A;Contents: annotation; Zie, revisions to residues 25, 59, 60, and 264-268  
A;Note: the revised sequence differs from that shown in having 60-Ala and in the amidat  
red

R;Milstein, C.; Frangione, B.  
Biochem. J. 121, 217-225, 1971  
A;Title: Disulphide bridges of the heavy chain of human immunoglobulin G2.  
A;Reference number: A90253; MUID:72033500; PMID:4940472  
A;Contents: annotation; myeloma protein Sa, disulfide bonds  
R;Frangione, B.; Milstein, C.; Pink, J.R.L.  
Nature 221, 145-148, 1969  
A;Title: Structural studies of immunoglobulin G.  
A;Reference number: A93157; MUID:69064124; PMID:5782707  
A;Contents: annotation; Sa, disulfide bonds  
C;Genetics:  
A;Gene: GDB:IGHG2  
A;Cross-references: GDB:119338; OMIM:147110  
A;Map position: 14q32.33-14q32.33  
C;Complex: An immunoglobulin heterotetramer subunit consists of two identical light (kap  
chain disulfide bonds. In some cases, such as IgA and IgM, the subunits associate into l  
C;Superfamily: immunoglobulin C region; immunoglobulin homology  
C;Keywords: duplication; glycoprotein; heterotetramer; immunoglobulin  
F;20-85/Domain: immunoglobulin homology <IM1>  
F;133-202/Domain: immunoglobulin homology <IM2>  
F;239-306/Domain: immunoglobulin homology <IM3>  
F;14/Disulfide bonds: interchain (to light chain) #status experimental  
F;27-83, 140-200, 246-304/Disulfide bonds: #status experimental  
F;102, 103, 106, 109/Disulfide bonds: interchain (to heavy chain) #status experimental  
F;176/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 87.9%; Score 1107; DB 1; Length 326;  
Best Local Similarity 88.4%; Pred. No. 2.8e-76;  
Matches 205; Conservative 12; Mismatches 11; Indels 4; Gaps 2;

Qy 1 EPKCDKTHTCPCPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
Db 99 ERKCCVE---CPCPCAPP-VAGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVQF 154

Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWNGKYEYCKVSKNKPAPIEKT 120  
Db 155 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSKNKPAPIEKT 214

Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEESGQPENNYKTP 180





RESULT 11  
I47160  
Ig gamma 2b chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47160  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47160  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03780; NID:G433125; PIDN:AAA52218.1; PID:G433126  
C:Genetics:  
A:Gene: IGG2b  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>  
  
Query Match 68.9%; Score 868.5; DB 2; Length 328;  
Best Local Similarity 70.1%; Pred. No. 2.8e-58;  
Matches 157; Conservative 32; Mismatches 3; Indels 3; Gaps 2;  
  
Qy 11 CPCCPAPELLGGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 70  
Db 106 CPICPACE-SFGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 164  
  
Qy 71 NVKTKPREQVNSTYRVSVLTVLHQNMNKGKCKVSNKALPAPIETISKAKVQPRE 130  
Db 165 TAQTRPKBEQNSTYRVSVLTVLHQNMNKGKCKVSNKALPAPIETISKAKVQPRE 224  
  
Qy 131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPPVLDVSGS 188  
Db 225 PQVYTLPPHAEELSRKSVITCLVIGFYPPDIDVEWQNGQPEPEGNYRTTTPQDQVDGT 284  
  
Qy 189 FFYLSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPK 232  
Db 285 YFLYSKFSVDKASWQGGIFQCAVMHEALHNHYTKSISKTPGK 328  
  
RESULT 12  
I47159  
Ig gamma 2a chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47159  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47159  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-328 <KAC>  
A:Cross-references: EMBL:U03779; NID:G433123; PIDN:AAA52217.1; PID:G433124  
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A:Gene: IGG2a  
C:Superfamily: immunoglobulin C region; immunoglobulin homology  
F:133-202/Domain: immunoglobulin homology <IMM>  
  
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Db 106 CPICPACE-SFGPSVFIFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKFNWYVDGVEVH 164  
  
Qy 71 NVKTKPREQVNSTYRVSVLTVLHQNMNKGKCKVSNKALPAPIETISKAKVQPRE 130  
Db 165 TAQTRPKBEQNSTYRVSVLTVLHQNMNKGKCKVSNKALPAPIETISKAKVQPRE 224  
  
Qy 131 PQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPPVLDVSGS 188  
Db 225 PQVYTLPPHAEELSRKSVITCLVIGFYPPDIDVEWQNGQPEPEGNYRTTTPQDQVDGT 284  
  
Qy 189 FFYLSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPK 232  
Db 285 YFLYSKFSVDKASWQGGIFQCAVMHEALHNHYTKSISKTPGK 328  
  
RESULT 13  
I47162  
Ig gamma 4 chain constant region - pig (fragment)  
C:Species: Sus scrofa domestica (domestic pig)  
C:Date: 21-Feb-1997 #sequence\_revision 21-Feb-1997 #text\_change 21-Jan-2000  
C:Accession: I47162  
R:Kacskovics, I.; Sun, J.; Butler, J.E.  
J. Immunol. 153, 3565-3573, 1994  
A:Title: Five putative subclasses of swine IgG identified from the cDNA sequences of a  
A:Reference number: I47158; MUID:95015845; PMID:7930579  
A:Accession: I47162  
A:Status: preliminary; translated from GB/EMBL/DDBJ  
A:Molecule type: mRNA  
A:Residues: 1-277 <KAC>  
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Db 109 GVEVHTAQTRPKBEQNSTYRVSVLTVLHQNMNKGKCKVSNKALPAPIETISKAK 168  
  
Qy 126 VQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQ--PENNYKTTTPPV 183  
Db 169 GQTRPEQVYTLPPTEELSRKSVITCLVIGFYPPDIDVEWQNGQPEPEGNYRTTTPQ 228  
  
Qy 184 DSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPK 232  
Db 229 DVDGTFFLYSKLAVDKASWQGGIFQCAVMHEALHNHYTKSISKTPGK 277  
  
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C:Species: Cavia porcellus (guinea pig)  
C:Date: 07-May-1981 #sequence\_revision 07-May-1981 #text\_change 09-Jul-2004  
C:Accession: A94553; A90352; A90359; A90384; A90385; A02151  
R:Trischmann, T.M.  
submitted to the Atlas, April 1975  
A:Reference number: A94553  
A:Accession: A94553  
A:Molecule type: protein  
A:Residues: 1-3 <TRI>  
A:Cross-references: UNIPROT:P01862  
R:Birshstein, B.K.; Hussain, Q.Z.; Cebra, J.J.  
Biochemistry 10, 18-25, 1971  
A:Title: Structure of heavy chain from strain 13 guinea pig immunoglobulin-G(2). III. Ar  
A:Reference number: A90352; MUID:71058471; PMID:5538606  
A:Accession: A90352  
A:Molecule type: protein  
A:Residues: 4-68 <BIR>  
R:Turner, K.J.; Cebra, J.J.

Db 165 TAQTRPKBEQNSTYRVSVLTVLHQNMNKGKCKVSNKALPAPIETISKAKVQPRE 224  
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Db 225 PQVYTLPPHAEELSRKSVITCLVIGFYPPDIDVEWQNGQPEPEGNYRTTTPQDQVDGT 284  
Qy 189 FFYLSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPK 232  
Db 285 YFLYSKFSVDKASWQGGIFQCAVMHEALHNHYTKSISKTPGK 328



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GenCore version 5.1.6  
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( protein - protein search, using sw model

in on: October 27, 2004, 16:32:53 ; Search time 105.267 Seconds  
(without alignments)  
1268.081 Million cell updates/sec

tle: US-10-000-439-3

rfect score: 1260

quence: 1 EPKSCDKTHTCPPAPPELL.....MHEALHHYQORSLSPGK 232

oring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

arched: 1825181 seqs, 575374646 residues

tal number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Maximum Match 0%

Maximum Match 100%

Listing first 45 summaries

atabase : UniProt 02.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1225	97.2	330	1 GCI HUMAN	P01857 homo sapien
2	1225	97.2	407	2 BAC85237	Bac85237 homo sapi
3	1225	97.2	447	2 BAC86226	Bac86226 homo sapi
4	1225	97.2	464	2 AAH19337	Aah19337 homo sapi
5	1225	97.2	465	2 Q6GMX6	Q6gmxx6 homo sapien
6	1225	97.2	466	2 Q6IN78	Q6in78 homo sapien
7	1225	97.2	466	2 AAH64496	Aah64496 homo sapi
8	1225	97.2	467	2 BAC85173	Bac85173 homo sapi
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20	1225	97.2	470	2 AAH25314	Aah25314 homo sapi
21	1225	97.2	471	2 BAC85388	Bac85388 homo sapi
22	1225	97.2	471	2 AAH24289	Aah24289 homo sapi
23	1225	97.2	471	2 BAC05014	Bac05014 homo sapi
24	1225	97.2	472	2 Q6N089	Q6n089 homo sapien
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27	1225	97.2	472	2 BAC86225	Bac86225 homo sapi
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RESULT 1

GCI HUMAN

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AC P01857;

DT 21-JUL-1986 (Rel. 01, Created)

DT 21-JUL-1986 (Rel. 01, Last sequence update)

DT 01-OCT-2004 (Rel. 45, Last annotation update)

DE I9 gamma-1 chain C region.

GN Name=IGHG1;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

SEQUENCE FROM N.A.

RP MEDLINE=82274238; PubMed=6287432;

RA Ellison J.W., Berson B.J., Hood L.E.;

RT "The nucleotide sequence of a human immunoglobulin C gamma1 gene.";

RL Nucleic Acids Res. 10:4071-4079(1982).

RN [2]

SEQUENCE OF 1-135 (MYELOMA PROTEIN EU).

RP MEDLINE=71064024; PubMed=5489771;

RA Cunningham B.A., Rutishauser U., Gall W.E., Gottlieb P.D.,

RA Waxdal M.J., Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. VII. Amino

acid sequence of heavy-chain cyanogen bromide fragments H1-H4.";

RL Biochemistry 9:3161-3170(1970).

RN [3]

SEQUENCE OF 136-329 (EU).

RP MEDLINE=71064025; PubMed=5530842;

RA Rutishauser U., Cunningham B.A., Bennett C., Konigsberg W.H.,

RA Edelman G.M.;

RT "The covalent structure of a human gamma G-immunoglobulin. 8. Amino

acid sequence of heavy-chain cyanogen bromide fragments H5-H7.";

RL Biochemistry 9:3171-3181(1970).

RN [4]

SEQUENCE (MYELOMA PROTEIN NIE).

RP MEDLINE=77070269; PubMed=826475;

RA Ponstingl H., Hilschmann N.;

RT "The rule of antibody structure. The primary structure of a monoclonal

IgG1 immunoglobulin (myeloma protein NIE). III. The chymotryptic

peptides of the H-chain, alignment of the tryptic peptides and

discussion of the complete structure.";

RL Hoppe-Seyler's Z. Physiol. Chem. 357:1571-1604(1976).

RN [5]

SEQUENCE (MYELOMA PROTEIN KOL), AND DISULFIDE BONDS.

RP MEDLINE=83289131; PubMed=6884994;

RA Schmidt W.E., Jung H.-D., Palm W., Hilschmann N.;

RT "Three-dimensional structure determination of antibodies. Primary

structure of crystallized monoclonal immunoglobulin IgG1 KOL, I.";

RL Hoppe-Seyler's Z. Physiol. Chem. 364:713-747(1983).

RN [6]

DISULFIDE BONDS.

RP MEDLINE=71064027; PubMed=4923144;

RN [7]

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RP MEDLINE=71064027; PubMed=4923144;

RN [8]

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RP MEDLINE=71064027; PubMed=4923144;

RN [9]

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RN [10]

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RP MEDLINE=71064027; PubMed=4923144;

RN [11]

DISULFIDE BONDS.

RP MEDLINE=71064027; PubMed=4923144;

RN [12]

DISULFIDE BONDS.

RA Gall W.E., Edelman G.M.;  
 RT "The covalent structure of a human gamma G-immunoglobulin. X.  
 RL Intrachain disulfide bonds.";  
 RN Biochemistry 9:3188-3196(1970).  
 RP [7]  
 RX DISULFIDE BONDS.  
 RA MEDLINE=77070267; PubMed=1002129;  
 RT Dreker L., Schwarz J., Reichel W., Hilschmann N.;  
 RT "Rule of antibody structure. The primary structure of a monoclonal  
 RT IgG1 immunoglobulin (myeloma protein Nie) I: purification and  
 RT characterization of the protein, the L- and H-chains, the cyanogen  
 RT bromide cleavage products, and the disulfide bridges.";  
 RL Hoppe-Seyler's Z. Physiol. Chem. 357:1515-1540(1976).  
 RN [8]  
 RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS).  
 RX MEDLINE=81208100; PubMed=7236608;  
 RA Deisenhofer J.;  
 RT "Crystallographic refinement and atomic models of a human Fc fragment  
 RT and its complex with fragment B of protein A from Staphylococcus  
 RT aureus at 2.9- and 2.8-A resolution.";  
 RL Biochemistry 20:2361-2370(1981).  
 CC -!- MISCELLANEOUS: Nie has the GIM(17) allotypic marker, 97-K, and the  
 CC GIM(1) markers, 239-D and 241-L. KOL and EU sequences have the  
 CC GIM(3) marker and the GIM (non-1) markers.  
 CC -!- MISCELLANEOUS: Nie also differs in the amidation states of 35,  
 CC 116, 198, 269 and 272.  
 CC -!- MISCELLANEOUS: EU also differs in the amidation states of residues  
 CC 155, 166, 177, 195, 198, 269, and 272 and in the order of residues  
 CC 268-272.  
 CC -!- MISCELLANEOUS: KOL also differs in the amidation states of  
 CC residues 198, 267 and 272.  
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 CC -----  
 DR EMBL; J00228; AAC82527.1; ALT\_INIT.  
 DR PIR; A93433; GHU.  
 DR PDB; 1AJ7; X-ray; H=1-103.  
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 DR PDB; 2RCS; X-ray; H=1-103.  
 DR Genew; HGNC:5525; IG\_HG1.  
 DR MIN; 147100; .  
 DR GO; GO:0005624; C:membrane fraction; NAS.  
 DR GO; GO:0003823; F:antigen binding; TAS.  
 DR GO; GO:0006955; P:immune response; NAS.  
 DR InterPro; IPR007110; Ig-like.  
 DR InterPro; IPR003006; Ig\_MHC.  
 DR Pfam; PF00047; ig; 3.  
 DR PROSITE; PS00835; IG\_LIKE; 3.  
 DR PROSITE; PS00290; IG\_MHC; 2.  
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 KW Immunoglobulin C region; Immunoglobulin domain.  
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 FT DOMAIN 99 110 Hinge.

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61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
RC TISSUE-Synovial membrane tissue;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanemori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.;
RT "NEDO human cDNA sequencing project.";
RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK125633; BAC86226.1;
SQ SEQUENCE 447 AA; 49289 MW; F28884C17E89B8EF CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 447;
Best Local Similarity 97.0%; Pred. No. 2.3e-89;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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QY 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
Db 276 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 335

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 336 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 395

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
Db 396 PVLDSGSGFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

RESULT 4
AAH19337
ID AAH19337 PRELIMINARY; PRT; 464 AA.
AC AAH19337;
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DT 02-VAR-2004 (TRENBLrel. 27, Last sequence update)
DT 02-VAR-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Masius K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.B., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuallano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).

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Query Match 97.2%; Score 1225; DB 2; Length 407;
Best Local Similarity 97.0%; Pred. No. 2.3e-89;
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b 236 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 295

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
b 296 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 355

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
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AC86226
D BAC86226 PRELIMINARY; PRT; 447 AA.
C BAC86226;
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T 02-VAR-2004 (TRENBLrel. 27, Last sequence update)
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E chain C region.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
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RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Synovial membrane tissue;
RA Tashiro H., Yamazaki M., Watanabe K., Kumagai A., Itakura S.,
RA Fukuzumi Y., Fujimori Y., Komiyama M., Sugiyama T., Irie R.,
RA Otsuki T., Sato H., Wakamatsu A., Ishii S., Yamamoto J., Isono Y.,
RA Kawai-Hio Y., Saito K., Nishikawa T., Kimura K., Yamashita H.,
RA Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K., Wagatsuma M.,
RA Murakawa K., Kanemori K., Takahashi-Fujii A., Oshima A., Sugiyama A.,
RA Kawakami B., Suzuki Y., Sugano S., Nagahari K., Masuho Y., Nagai K.,
RA Isogai T.;
RT "NEDO human cDNA sequencing project.";
RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK125633; BAC86226.1;
SQ SEQUENCE 447 AA; 49289 MW; F28884C17E89B8EF CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 447;
Best Local Similarity 97.0%; Pred. No. 2.3e-89;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
Db 216 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 275

QY 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120
Db 276 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 335

QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180
Db 336 ISKAKGQPREPOVYTLPPSRDELTKNOVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 395

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 232
Db 396 PVLDSGSGFFLYSKLTVDKSRWQGNVFSCSVMHEALHNHYTQKSLSLSPGK 447

RESULT 4
AAH19337
ID AAH19337 PRELIMINARY; PRT; 464 AA.
AC AAH19337;
DT 02-VAR-2004 (TRENBLrel. 27, Created)
DT 02-VAR-2004 (TRENBLrel. 27, Last sequence update)
DT 02-VAR-2004 (TRENBLrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Primary B-Cells;
RC MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.P., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Masius K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.B., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Locuallano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smalls D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16999-16903 (2002).

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[2]  
 RN SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC019337; AAH19337.1; --  
 KW Hypothetical protein.  
 SQ SEQUENCE 464 AA; 50891 MW; 2F80673E74E2A485 CRC64;  
 Query Match 97.2%; Score 1225; DB 2; Length 464;  
 Best Local Similarity 97.0%; Pred. No. 2.7e-89;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 Db 233 EPKSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 292  
 QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120  
 Db 293 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT 352  
 QY 121 ISKAKVQPREPVVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180  
 Db 353 ISKAKGQPREPVVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 412  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232  
 Db 413 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 464  
 RESULT 5  
 Q6GMX6  
 ID Q6GMX6 PRELIMINARY; PRT; 465 AA.  
 AC Q6GMX6;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Sherman C.M., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Primary B-Cells;  
 RA Strausberg R.;  
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC073766; AAH73766.1; --  
 KW InterPro; IPR003599; 1g.

DR InterPro; IPR007110; 1g-like.  
 DR InterPro; IPR003597; 1g\_c1.  
 DR InterPro; IPR003006; 1g\_MHC.  
 DR InterPro; IPR003596; 1g\_v.  
 DR Pfam; PF07654; C1-set; 3.  
 DR Pfam; PF00047; 1g; 4.  
 DR SMART; SM00409; 1g; 2.  
 DR SMART; SM00407; 1g; 3.  
 DR SMART; SM00406; 1g; 1.  
 DR PROSITE; PS00835; 1g\_LIKE; 4.  
 DR PROSITE; PS00290; 1g\_MHC; UNKNOWN\_2.  
 KW Hypothetical protein\_1386E.  
 SQ SEQUENCE 465 AA; 51083 MW; B3A9B7D0FDB1386E CRC64;  
 Query Match 97.2%; Score 1225; DB 2; Length 465;  
 Best Local Similarity 97.0%; Pred. No. 2.7e-89;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 Db 234 EPKSCDKTHCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 293  
 QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNMNGKEYCKVSNKALPAPIEKT 120  
 Db 294 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDMLNGKEYCKVSNKALPAPIEKT 353  
 QY 121 ISKAKVQPREPVVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 180  
 Db 354 ISKAKGQPREPVVTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTP 413  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232  
 Db 414 PVLDSGDSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 465  
 RESULT 6  
 Q6IN78  
 ID Q6IN78 PRELIMINARY; PRT; 466 AA.  
 AC Q6IN78;  
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)  
 DE IGHL1 protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE=Peripheral Nervous System;  
 RX MEDLINE=22388257; PubMed=12477932;  
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Sherman C.M., Schuler G.D.,  
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 RA Bobak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Shevchenko Y., Bouffard G.G.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,  
 RA Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RT and mouse cDNA sequences.";  
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RN [2]



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SEQUENCE FROM N.A.
TISSUE=Peripheral Nervous System;
Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
EMBL; BC072419; AAH72419.1; -.
InterPro; IPR003599; IG.
InterPro; IPR007110; IG-like.
InterPro; IPR003597; IG c1.
InterPro; IPR003006; IG_MHC.
InterPro; IPR003596; IG_V.
Pfam; PF07654; Cl-set; 3.
Pfam; PF00047; IG; 4.
SMART; SM00409; IG; 2.
SMART; SM00407; IGc1; 3.
SMART; SM00406; IGV; 1.
PROSITE; PS0835; IG LIKE; 4.
PROSITE; PS0290; IG_MHC; UNKNOWN 2.
SEQUENCE 466 AA; 50853 MW; 53EB08CEDE81075E CRC64;

Query Match          97.2%; Score 1225; DB 2; Length 466;
Best Local Similarity 97.0%; Pred. No. 2.7e-89;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

/ 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
/ 235 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 294

/ 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
/ 295 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 354

/ 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTP 180
/ 355 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTP 414

/ 181 PVLDSGSGFFLYSKLTVDKSRWQGNVFSCVMEALHNHYQOQSLSLSPGK 232
/ 415 PVLDSGSGFFLYSKLTVDKSRWQGNVFSCVMEALHNHYQOQSLSLSPGK 466

RESULT 7
AAH64496 PRELIMINARY; PRT; 466 AA.
AAH64496
/ 02-MAR-2004 (TRENBLrel. 27, Created)
/ 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
/ 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
E Hypothetical protein.
S Homo sapiens (Human).
C Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
C Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
X NCBI_TaxID=9606;
N [1]
SEQUENCE FROM N.A.
TISSUE=Spleen;
MEDLINE=22388257; PubMed=12477932;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
Villalón D.K., Muny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodríguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
Krzyszinski M.I., Skalska U., Smailus D.E., Scherch A., Schein J.E.,
Jones S.J., Marra M.A.
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RT "Generation and initial analysis of more than 15,000 full-length human
RT and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Spleen;
RA Strausberg R.;
RL Submitted (DEC-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC064496; AAH64496.1; -.
KW Hypothetical protein.
SQ SEQUENCE 466 AA; 51078 MW; 13F032EDAC9DBC22 CRC64;

Query Match          97.2%; Score 1225; DB 2; Length 466;
Best Local Similarity 97.0%; Pred. No. 2.7e-89;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 235 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 294

QY 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
DB 295 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 354

QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTP 180
DB 355 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTP 414

QY 181 PVLDSGSGFFLYSKLTVDKSRWQGNVFSCVMEALHNHYQOQSLSLSPGK 232
DB 415 PVLDSGSGFFLYSKLTVDKSRWQGNVFSCVMEALHNHYQOQSLSLSPGK 466

RESULT 8
BAC85173 PRELIMINARY; PRT; 467 AA.
AC BAC85173
DT 02-MAR-2004 (TRENBLrel. 27, Created)
DT 02-MAR-2004 (TRENBLrel. 27, Last sequence update)
DT 02-MAR-2004 (TRENBLrel. 27, Last annotation update)
DE CDNA FLJ26001 fis, clone DMC07585, highly similar to Ig gamma-1 chain
DE C region.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dermod tumor;
RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RA "NEDO human cDNA sequencing project.";
RT Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
RL EMBL; AK129512; BAC85173.1; -.
SQ SEQUENCE 467 AA; 50782 MW; 632AEA2D6CD248F5 CRC64;

Query Match          97.2%; Score 1225; DB 2; Length 467;
Best Local Similarity 97.0%; Pred. No. 2.7e-89;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 60
DB 236 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVDVSHEDPEVKF 295

QY 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120
DB 296 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 355

QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTP 180
DB 356 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGYFSPDSIAVEWESNGQPENNYKTTTP 415
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QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQORSLSLSPGK 232
DB 416 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPGK 467

RESULT 9
AAH37361
ID AAH37361 PRELIMINARY; PRT; 467 AA.
AC AAH37361;
DT 02-MAR-2004 (Tremblrel. 27, Created)
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A.C., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Splice;
RA Strausberg R.;
RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC037361; AAH37361.1; -.
KW Hypothetical protein.
SQ SEQUENCE 467 AA; 51129 MW; 20F0F71415B25B48 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 467;
Best Local Similarity 97.0%; Pred. No. 2.7e-89;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 236 EPKSCDKTHTCPCPAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKF 295

QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNWNGKEYCKVSNKALPAPIEKT 120
DB 296 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 355

QY 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 356 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 415

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQORSLSLSPGK 232
DB 416 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPGK 467

RESULT 10
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ID AAH37361 PRELIMINARY; PRT; 467 AA.
AC AAH37361;
DT 02-MAR-2004 (Tremblrel. 27, Created)
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
DE Hypothetical protein.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
RA Sugano S.;
RT "NEDO human cDNA sequencing project."
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK130844; BAC85444.1; -.
SQ SEQUENCE 468 AA; 51224 MW; 9280ACAD6817FC20 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 468;
Best Local Similarity 97.0%; Pred. No. 2.7e-89;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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BAC85175
ID BAC85175 PRELIMINARY; PRT; 468 AA.
AC BAC85175;
DT 02-MAR-2004 (Tremblrel. 27, Created)
DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
DE CDNA FLJ26006 fis, clone DMC08725, highly similar to Ig gamma-1 chain
C region.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Dermod tumor;
RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,
RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,
RA Kawakami B., Nagai K., Isogai T., Sugano S.;
RT "NEDO human cDNA sequencing project."
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK129517; BAC85175.1; -.
SQ SEQUENCE 468 AA; 51266 MW; 11C519D86AE3D44B CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 468;
Best Local Similarity 97.0%; Pred. No. 2.7e-89;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPCPAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 237 EPKSCDKTHTCPCPAPPELLGGPSVFLPFPKDTLMISRTPEVTCVVVDVSHEDPEVKF 296

QY 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQNWNGKEYCKVSNKALPAPIEKT 120
DB 297 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 356

QY 121 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
DB 357 ISKAKQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 416

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQORSLSLSPGK 232
DB 417 PVLDSGDSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTKSLSLSPGK 468

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ID BAC85444 PRELIMINARY; PRT; 468 AA.
AC BAC85444;
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DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)
DE CDNA FLJ27334 fis, clone TMS09201, highly similar to Ig gamma-1 chain
C region.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Thymus;
RA Kawakami B., Sugiyama A., Takemoto M., Suzuki Y., Hata H.,
RA Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Sugiyama T.,
RA Irie R., Otsuki T., Sato H., Nishikawa T., Nagai K., Isogai T.,
RA Sugano S.;
RT "NEDO human cDNA sequencing project."
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK130844; BAC85444.1; -.
SQ SEQUENCE 468 AA; 51224 MW; 9280ACAD6817FC20 CRC64;

Query Match 97.2%; Score 1225; DB 2; Length 468;
Best Local Similarity 97.0%; Pred. No. 2.7e-89;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

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 237 EPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 236  
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 297 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNWMNGKVKCKVSNKALPAPIEKT 356  
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 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
 3 IGHG1 protein.  
 3 Homo sapiens (Human).  
 3 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 3 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 3 NCBI\_TaxID=9606;  
 3 [1]  
 3 SEQUENCE FROM N.A.  
 3 TISSUE=Spleen;  
 3 MEDLINE=22388257; PubMed=12477932;  
 3 Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
 3 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 3 Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 3 Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 3 Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 3 Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
 3 Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
 3 Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,  
 3 Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 3 Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 3 Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 3 Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 3 Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 3 Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 3 Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.B.,  
 3 Jones S.J., Marra M.A.;  
 3 "Generation and initial analysis of more than 15,000 full-length human  
 3 and mouse cDNA sequences.";  
 3 Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 3 [2]  
 3 SEQUENCE FROM N.A.  
 3 TISSUE=Spleen;  
 3 Strausberg R.;  
 3 Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.  
 3 EMBL; BC051328; AAH51328.1; -  
 3 InterPro; IPR007110; IG-like.  
 3 InterPro; IPR003597; IG-cl.  
 3 InterPro; IPR003006; IG-MHC.  
 3 InterPro; IPR003596; IG-v.  
 3 Pfam; PF07654; CI-set; 3.  
 3 Pfam; PF00047; IG; 1.  
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 3 PROSITE; PS00835; IG-LIKE; 4.  
 3 PROSITE; PS00290; IG-MHC; UNKNOWN 2.  
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Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
 DB 237 EPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 297  
 QY 61 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNWMNGKVKCKVSNKALPAPIEKT 120  
 DB 297 NWYVDGVEVHNKTPREEQNSTYRVVSVLTVLHQNWMNGKVKCKVSNKALPAPIEKT 357  
 QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
 DB 357 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 417  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYHQORSLSLSPGK 232  
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 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)  
 DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)  
 DE Hypothetical protein.  
 DE Hypothetical protein.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
 OC NCBI\_TaxID=9606;  
 RN [1]  
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 RC TISSUE=Primary B-Cells;  
 RX MEDLINE=22388257; PubMed=12477932;  
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 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,  
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,  
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,  
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,  
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 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
 RA Villalón D.K., Muzny K.C., Sodergren E.J., Lu X., Gibbs R.A.,  
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,  
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
 RA Krzywinski M.I., Skalska U., Smallus D.E., Schnerch A., Schein J.B.,  
 RA Jones S.J., Marra M.A.;  
 RA "Generation and initial analysis of more than 15,000 full-length human  
 RA and mouse cDNA sequences.";  
 RA Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).  
 RL [2]  
 RN SEQUENCE FROM N.A.  
 RP TISSUE=Primary B-Cells;  
 RC Strausberg R.;  
 RL Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.  
 DR EMBL; BC018747; AAH18747.1; -  
 DR InterPro; IPR003599; IG.  
 DR InterPro; IPR007110; IG-like.  
 DR InterPro; IPR003597; IG-cl.  
 DR InterPro; IPR003006; IG-MHC.  
 DR InterPro; IPR003596; IG-v.  
 DR Pfam; PF07654; CI-set; 3.  
 DR Pfam; PF00047; IG; 4.  
 DR SMART; SM00409; IG; 2.  
 DR SMART; SM00407; IGC1; 3.  
 DR SMART; SM00406; IGV; 1.  
 DR PROSITE; PS00835; IG-LIKE; 4.  
 DR PROSITE; PS00290; IG-MHC; UNKNOWN 2.

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Best Local Similarity 97.0%; Pred. No. 2.7e-89;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 239 EPKSCDKTHTCPCPAPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 298  
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120  
DB 299 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358  
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
DB 359 ISKAKGQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 418  
QY 181 PVLDVSGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232  
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DT 01-OCT-2003 (Tremblrel. 25, Last sequence update)  
DT 01-MAR-2004 (Tremblrel. 26, Last annotation update)  
DE Hypothetical protein.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
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RX MEDLINE=2238257; PubMed=12477932;  
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,  
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,  
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RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,  
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullány S.J.,  
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,  
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,  
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,  
RA Fahey J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,  
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,  
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,  
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,  
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerk A., Schein J.E.,  
RA Jones S.J., Marra M.A.;  
RT "Generation and initial analysis of more than 15,000 full-length human  
RT and mouse cDNA sequences";  
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).  
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RC TISSUE=Spleen;  
RA Strausberg R.;  
RL Submitted (JUN-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; BC053984; AAH51984.1; -  
DR InterPro; IPR007110; IG-like.  
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DR InterPro; IPR003006; IG\_MHC.  
DR InterPro; IPR003596; IG\_v.  
DR Pfam; PF07654; CI-set; 3.  
DR Pfam; PF00047; IG; 1.  
DR SMART; SM00406; IGV; 1.

DR PROSITE; PS00835; IG-LIKE; 4.  
DR PROSITE; PS00290; IG-MHC; UNKNOWN\_2.  
KW Hypothetical protein.  
SQ SEQUENCE 470 AA; 51204 MW; 778CF34521483E1A CRC64;  
Query Match 97.2%; Score 1225; DB 2; Length 470;  
Best Local Similarity 97.0%; Pred. No. 2.7e-89;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60  
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DT 02-MAR-2004 (Tremblrel. 27, Last sequence update)  
DT 02-MAR-2004 (Tremblrel. 27, Last annotation update)  
DE CDNA FLJ26276 fis, clone DMC06522, highly similar to Ig gamma-1 chain  
DE C region.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo.  
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RC TISSUE=Dermoid tumor;  
RA Ota T., Nakagawa S., Senoh A., Mizuguchi H., Inagaki H., Suzuki Y.,  
RA Hata H., Nakagawa K., Mizuno S., Morinaga M., Kawamura M.,  
RA Sugiyama T., Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A.,  
RA Kawakami B., Nagai K., Isogai T., Sugano S.;  
RT "XEDO human cDNA sequencing project";  
RL Submitted (JUL-2003) to the EMBL/GenBank/DBJ databases.  
DR EMBL; AK129787; BAC85235.1; -  
SQ SEQUENCE 470 AA; 51090 MW; 460F4717D4528A16 CRC64;  
Query Match 97.2%; Score 1225; DB 2; Length 470;  
Best Local Similarity 97.0%; Pred. No. 2.7e-89;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHTCPCPAPELLGGPSVFLFPPPKDITLMISRTPEVTCVVVDVSHEDPEVKF 60  
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QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120  
DB 299 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 358  
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QY 181 PVLDVSGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNNHYQORSLSLSPGK 232  
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GenCore version 5.1.6  
Copyright (c) 1993 - 2004 Compugen Ltd.

1 protein - protein search, using sw model

in on: October 27, 2004, 16:31:18 ; Search time 88.7544 Seconds  
(without alignments)  
937.702 Million cell updates/sec

file: US-10-000-439-3

sequence: 1 EPKSCDTHRCPCPAPELL.....MHEALHHYQQRSLSPCK 232

oring table: BLOSUM62

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arched: 2002273 seqs, 358729299 residues

tal number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

st-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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1: Geneseq1980s:\*  
2: Geneseq1990s:\*  
3: Geneseq2000s:\*  
4: Geneseq2001s:\*  
5: Geneseq2002s:\*  
6: Geneseq2003as:\*  
7: Geneseq2003bs:\*  
8: Geneseq2004s:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1260	100.0	330	AAO19664	Aao19664 Human Igg
3	1260	100.0	569	AAO19668	Aao19668 GE2 fusio
4	1225	97.2	232	AAW26232	Aaw26232 Human Igg
5	1225	97.2	232	AAW26232	Aaw26232 Human Igg
6	1225	97.2	232	AAW26232	Aaw26232 Human Igg
7	1225	97.2	232	AAW26232	Aaw26232 Human Igg
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11	1225	97.2	232	AAW26232	Aaw26232 Human Igg
12	1225	97.2	232	AAW26232	Aaw26232 Human Igg
13	1225	97.2	232	AAW26232	Aaw26232 Human Igg
14	1225	97.2	232	AAW26232	Aaw26232 Human Igg
15	1225	97.2	232	AAW26232	Aaw26232 Human Igg
16	1225	97.2	232	AAW26232	Aaw26232 Human Igg
17	1225	97.2	232	AAW26232	Aaw26232 Human Igg
18	1225	97.2	232	AAW26232	Aaw26232 Human Igg
19	1225	97.2	232	AAW26232	Aaw26232 Human Igg
20	1225	97.2	232	AAW26232	Aaw26232 Human Igg
21	1225	97.2	232	AAW26232	Aaw26232 Human Igg
22	1225	97.2	232	AAW26232	Aaw26232 Human Igg
23	1225	97.2	232	AAW26232	Aaw26232 Human Igg
24	1225	97.2	232	AAW26232	Aaw26232 Human Igg
25	1225	97.2	232	AAW26232	Aaw26232 Human Igg

26	1225	97.2	330	5	AAW47856	Aam47856 Human Igg
27	1225	97.2	330	5	AAE21960	Aae21960 Human Igg
28	1225	97.2	330	5	ABB81641	Abb81641 Human Igg
29	1225	97.2	330	5	ABB05736	Abb05736 Human Igg
30	1225	97.2	330	6	ABP71856	Abp71856 Human Igg
31	1225	97.2	330	6	AAE32915	Aae32915 Human Igg
32	1225	97.2	330	6	AAE32627	Aae32627 Human Igg
33	1225	97.2	330	6	ABR82103	Abr82103 Human Igg
34	1225	97.2	330	6	AAO31102	Aao31102 Human Igg
35	1225	97.2	330	6	ABR55836	ABr55836 Anti-Ang
36	1225	97.2	330	6	AAO30893	Aao30893 Human Igg
37	1225	97.2	330	7	ADFI1389	Adfi1389 Anti-OPGL
38	1225	97.2	330	7	ADFI1389	Adfi1389 Anti-OPGL
39	1225	97.2	330	7	ADF83605	Adf83605 Cytokine
40	1225	97.2	330	7	ADF75001	Adf75001 Human Igg
41	1225	97.2	330	8	ADM41537	Adm41537 Anti-inte
42	1225	97.2	330	8	ADM68911	Adm68911 Human Igg
43	1225	97.2	330	8	ADN36570	Adn36570 Chemokine
44	1225	97.2	330	8	ADN97485	Adn97485 Artificia
45	1225	97.2	331	3	AAW91106	Aay91106 Human TR-

ALIGNMENTS

RESULT 1  
AAO19665  
ID AAO19665 standard; protein; 232 AA.

AC AAO19665;

DT 28-MAR-2003 (first entry)

DE Human IgG1 heavy chain constant region hinge-CH2-CH3 portion.

KW Human; IgG1; immunoglobulin G; immunotherapy; immune disease;  
KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;  
KW antiasthmatic; antiallergic; antiinflammatory; dermatological;  
KW antiarthritic; antirheumatic; antidiabetic; neuroprotective;  
KW hinge-CH2-CH3 region.

OS Homo sapiens.

XX WO200288317-A2.

PD 07-NOV-2002.

PF 01-MAY-2002; 2002WO-US013527.

PR 01-MAY-2001; 2001US-00847208.

XX 24-OCT-2001; 2001US-00000439.

PA (REGC ) UNIV CALIFORNIA.

PI Saxon A, Zhang K, Zhu D;

XX WPI; 2003-103456/09.

DR New fusion molecules comprising polypeptide sequences that bind to IgG  
inhibitory receptor and native IgE receptor, useful for treating IgE-  
mediated hypersensitivity reactions, e.g. asthma or allergies, or  
autoimmune diseases.

PS Claim 19; Fig 3; 116pp; English.

XX The present invention relates to a fusion molecule comprising a first  
polypeptide sequence capable of specific binding to a native IgG  
inhibitory receptor consisting of an immune receptor tyrosine-based  
inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
functionally connected to a second polypeptide sequence capable of  
specific binding directly or indirectly to a native IgE receptor  
(Fc epsilon receptor). Also provided are nucleotide sequences encoding such a  
fusion protein. The fusion molecules and compositions are useful for

CC treating an IgE-mediated biological response, preferably an IgE-mediated  
 CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
 CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
 CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
 CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,  
 CC or symptoms resulting from, a type I hypersensitivity reaction in a  
 CC subject receiving immunotherapy. The present sequence is the human IgG1  
 CC heavy chain constant region hinge-CH2-CH3 portion  
 XX  
 SQ Sequence 232 AA;

Query Match 100.0%; Score 1260; DB 6; Length 232;  
 Best Local Similarity 100.0%; Pred. No. 2.8e-91;  
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
 DB 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
 QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLTQHWMMNGEKYCKVSNKALPAPIEKT 120  
 DB 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLTQHWMMNGEKYCKVSNKALPAPIEKT 120  
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 DB 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQORSLSLSPGK 232  
 DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQORSLSLSPGK 232

RESULT 2  
 AAO19664  
 ID AAO19664 standard; protein; 330 AA.  
 XX  
 AC AAO19664;  
 XX  
 DT 28-MAR-2003 (first entry)  
 XX  
 DE Human IgG1 heavy chain constant region.  
 XX  
 KW Human; IgG1; immunoglobulin G; immunotherapy; immune disease;  
 KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;  
 KW antiasthmatic; anti-allergic; anti-inflammatory; dermatological;  
 KW antiarthritic; antirheumatic; antidiabetic; neuroprotective.  
 XX  
 OS Homo sapiens.  
 XX  
 FN WO200288317-A2.  
 XX  
 PD 07-NOV-2002.  
 XX  
 PF 01-MAY-2002; 2002WO-US013527.  
 XX  
 PR 01-MAY-2001; 2001US-00847208.  
 XX  
 PR 24-OCT-2001; 2001US-00000439.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Saxon A, Zhang K, Zhu D;  
 XX  
 DR WPI; 2003-103456/09.  
 XX  
 PT New fusion molecules comprising polypeptide sequences that bind to IgG  
 PT inhibitory receptor and native IgE receptor, useful for treating IgE-  
 PT mediated hypersensitivity reactions, e.g. asthma or allergies, or  
 PT autoimmune diseases.  
 XX  
 PS Claim 64; Fig 2; 116pp; English.  
 XX  
 CC The present invention relates to a fusion molecule comprising a first  
 CC polypeptide sequence capable of specific binding to a native IgG

CC inhibitory receptor consisting of an immune receptor tyrosine-based  
 CC inhibitory motif (ITIM), expressed on mast cells, basophils or B cells,  
 CC functionally connected to a second polypeptide sequence capable of  
 CC specific binding directly or indirectly to a native IgE receptor  
 CC (Fc epsilonR). Also provided are nucleotide sequences encoding such a  
 CC fusion protein. The fusion molecules and compositions are useful for  
 CC treating an IgE-mediated biological response, preferably an IgE-mediated  
 CC hypersensitivity reaction, such as asthma, allergic rhinitis, atopic  
 CC dermatitis, severe food allergies, chronic urticaria, angioedema or  
 CC anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis,  
 CC type-I diabetes mellitus, or multiple sclerosis, and for preventing of,  
 CC or symptoms resulting from, a type I hypersensitivity reaction in a  
 CC subject receiving immunotherapy. The present sequence is the human IgG1  
 CC heavy chain constant region  
 XX  
 SQ Sequence 330 AA;

Query Match 100.0%; Score 1260; DB 6; Length 330;  
 Best Local Similarity 100.0%; Pred. No. 4.2e-91;  
 Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
 DB 99 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 158  
 QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLTQHWMMNGEKYCKVSNKALPAPIEKT 120  
 DB 159 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLTQHWMMNGEKYCKVSNKALPAPIEKT 218  
 QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 DB 219 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 278  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQORSLSLSPGK 232  
 DB 279 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNYQORSLSLSPGK 330

RESULT 3  
 AAO19668  
 ID AAO19668 standard; protein; 569 AA.  
 XX  
 AC AAO19668;  
 XX  
 DT 28-MAR-2003 (first entry)  
 XX  
 DE GE2 fusion protein for use in treating immune diseases.  
 XX  
 KW Human; IgE; immunoglobulin E; immunotherapy; immune disease;  
 KW Fc epsilon receptor; autoimmune disease; constant region; heavy chain;  
 KW antiasthmatic; anti-allergic; anti-inflammatory; dermatological; GE2;  
 KW antiarthritic; antirheumatic; antidiabetic; neuroprotective;  
 KW fusion protein.  
 XX  
 OS Synthetic.  
 OS Unidentified.  
 XX  
 FN WO200288317-A2.  
 XX  
 PD 07-NOV-2002.  
 XX  
 PF 01-MAY-2002; 2002WO-US013527.  
 XX  
 PR 01-MAY-2001; 2001US-00847208.  
 XX  
 PR 24-OCT-2001; 2001US-00000439.  
 XX  
 PA (REGC ) UNIV CALIFORNIA.  
 XX  
 PI Saxon A, Zhang K, Zhu D;  
 XX  
 DR WPI; 2003-103456/09.  
 XX  
 PT New fusion molecules comprising polypeptide sequences that bind to IgG



inhibitory receptor and native IgE receptor, useful for treating IgE-mediated hypersensitivity reactions, e.g. asthma or allergies, or autoimmune diseases.

Claim 35; Fig 7; 116pp; English.

The present invention relates to a fusion molecule comprising a first polypeptide sequence capable of specific binding to a native IgG inhibitory receptor consisting of an immune receptor tyrosine-based inhibitory motif (ITIM), expressed on mast cells, basophils or B cells, functionally connected to a second polypeptide sequence capable of specific binding directly or indirectly to a native IgE receptor (FcεRI). Also provided are nucleotide sequences encoding such a fusion protein. The fusion molecules and compositions are useful for treating an IgE-mediated biological response, preferably an IgE-mediated hypersensitivity reaction, such as asthma, allergic rhinitis, atopic dermatitis, severe food allergies, chronic urticaria, angioedema or anaphylactic shock; or autoimmune diseases such as rheumatoid arthritis, type-1 diabetes mellitus, or multiple sclerosis, and for preventing of, or symptoms resulting from, a type I hypersensitivity reaction in a subject receiving immunotherapy. The present invention is a gammahinge-CHgamma2-CHgamma3- (Gly4Ser)3-Chepsilon2-Chepsilon3-CHepsilon3 fusion protein (designated GE2) of the invention

Sequence 569 AA;

Query Match 100.0%; Score 1260; DB 6; Length 569;

Best Local Similarity 100.0%; Pred. No. 8.1e-91;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EPKCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

1 EPKCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

61 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120

61 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120

121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180

121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180

181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYQQRSLSPGK 232

181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYQQRSLSPGK 232

RESULT 4

AW26232

AAW26232 standard; protein; 232 AA.

AAW26232;

16-MAR-1998 (first entry)

Human IgG1 hinge/Fc region.

Fusion protein; hydrophilic spacer; recombinant; expression system; carboxypeptidase; IgG1; immunoglobulin; hinge region; Fc.

Homo sapiens.

WO9728272-A1.

07-AUG-1997.

31-JAN-1997; 97WO-US001470.

31-JAN-1996; 96US-00595043.

(TECH-) TECHNOLOGENE INC.

Sgarlato GD;

XX WPI; 1997-402624/37.

XX N-PSDB; AAT80158.

XX Recombinant protein expression system for fusion protein production - useful for high quantity production of authentic recombinant proteins.

XX Example 3; Page 133-134; 194pp; English.

XX A novel recombinant vector has been developed which comprises a nucleotide sequence encoding a fusion protein. The fusion protein comprises three domains joined together in order, from N-terminus to C-terminus, of a first domain comprising a protein of interest, a second domain comprising a hydrophilic spacer and an affinity domain, each domain comprising amino acid residues. The present sequence represents the hinge/Fc region of human IgG1, used in example 3 of the present invention. The recombinant vector is used for the production of authentic recombinant proteins of interest. The method of the invention is useful for the expression of fusion proteins capable of isolation by affinity chromatography in pro- or eukaryotic cells. This method allows for the efficient cleavage and generation of authentic proteins of interest that do not contain extraneous (i.e. non-naturally occurring) amino acids

XX Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 2; Length 232;

Best Local Similarity 97.0%; Pred. No. 1.6e-88;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

Db 1 EPKCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120

Db 61 NWYVDGVEVHNKTKPREEQYNSTYRVSVLTVLHQNWMNGKEYCKVSNKALPAPIEKT 120

QY 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180

Db 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180

QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYQQRSLSPGK 232

Db 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFSCVMHEALHNHYQQRSLSPGK 232

RESULT 5

AAB28690

AAB28690 standard; protein; 232 AA.

AC AAB28690;

DT 14-FEB-2001 (first entry)

Human IgGammal hinge, CH2 and CH3 regions.

Human; AGP-1; type II transmembrane protein; cytostatic; antiviral; antiinflammatory; hepatotropic; antiarteriosclerotic; anti-HIV; HIV; human immunodeficiency virus; apoptosis; proliferative disorder; cancer; hepatitis; acquired immunodeficiency syndrome; AIDS; autoimmune disorder; transplant rejection; cardiovascular disease; arteriosclerosis; IgGammal.

OS Homo sapiens.

XX WO200063253-A1.

XX 26-OCT-2000.

XX 24-MAR-2000; 2000WO-US008004.

XX 16-APR-1999; 99US-00293245.

PA (AMGE-) AMGEN INC.  
 XX PI Hsu H, Meng S;  
 XX WPI; 2000-665240/64.  
 XX Fusing protein of ACP-1 protein and an Fc region, used to treat  
 PT proliferative disorders, immune disorders, and virally-induced disorders.  
 XX PS Claim 2; Fig 1; 93pp; English.  
 XX CC The present sequence was used in the production of ACP-1 fusion proteins.  
 CC ACP-1 is a type II transmembrane protein. The fusion proteins comprise an  
 CC Fc immunoglobulin region fused to the N-terminal portion of the ACP-1  
 CC protein. The fusion proteins can be used to induce apoptosis in a tissue,  
 CC and to treat proliferative disorders, immune disorders, or virally-  
 CC induced disorders. The proliferative disorders include cancers, such as  
 CC breast, prostate, lung or colon cancer. The viral infections include  
 CC hepatitis, and acquired immunodeficiency syndrome (AIDS), and the immune  
 CC disorders may be autoimmune disorders or transplant rejection.  
 CC Cardiovascular diseases such as arteriosclerosis may also be treated. The  
 CC ACP-1 containing fusion proteins have increased biological activity  
 CC compared to the soluble ACP-1 proteins used in prior art therapies  
 XX SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 3; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 1.6e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 DB 1 EPKSCDKHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKCKVSNKALPAPIEKT 120  
 DB 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKCKVSNKALPAPIEKT 120  
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232  
 DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 6  
 AAB80897  
 ID AAB80897 standard; protein; 232 AA.  
 AC AAB80897;  
 XX 31-MAY-2001 (first entry)  
 DT Human IgGammal hinge, CH2 and CH3 regions.  
 DE Human; IgGammal; anticancer; Antimetastatic; Osteogenic;  
 XX lytic bone disease; multiple myeloma; immunoglobulin;  
 KW osteoclastic bone metastasis; OPG; osteoprotegerin;  
 KW osteoclast formation inhibition; bone resorption inhibition.  
 XX Homo sapiens.  
 OS WO200117543-A2.  
 XX 15-MAR-2001.  
 PD 18-AUG-2000; 2000WO-US022806.  
 XX 03-SEP-1999; 99US-00389545.  
 XX (AMGE-) AMGEN INC.  
 PA

XX Dunstan CR;  
 XX WPI; 2001-265936/27.  
 XX Preventing or treating lytic bone diseases, particularly associated with  
 PT cancer or metastasis, by administering an osteoprotegerin polypeptide.  
 XX PS Disclosure; Fig 1; 87pp; English.  
 XX CC The present invention relates to a method for the prevention or treatment  
 CC of lytic bone disease or multiple myeloma. Also the method can be used  
 CC for preventing metastasis of cancer to bone or osteosclerotic bone  
 CC metastasis. The method comprises administering an OPG (osteoprotegerin)  
 CC polypeptide or OPG fusion protein. The OPG proteins (see AAB80898-  
 CC AAB80905) can inhibit formation of osteoclasts (and thus bone resorption)  
 CC by blocking differentiation from monocytes/macrophage precursors. The  
 CC present sequence is the hinge, CH2 and CH3 regions of human IgGammal.  
 CC This sequence can be used to generate fusion proteins of OPG and  
 CC immunoglobulin, for use in the present invention. The generated fusion  
 CC proteins can exhibit increased circulating half-lives and slower  
 CC clearance times, thereby providing a more sustained activity  
 XX SQ Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 4; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 1.6e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 DB 1 EPKSCDKHTCCPCAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKCKVSNKALPAPIEKT 120  
 DB 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDNMNGKEYCKCKVSNKALPAPIEKT 120  
 QY 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 DB 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232  
 DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

RESULT 7  
 AAY72915  
 ID AAY72915 standard; protein; 232 AA.  
 AC AAY72915;  
 XX 13-JUN-2001 (first entry)  
 DT Human partial IgG1 protein comprising hinge, CH2 and CH3 regions.  
 DE Human; fusion protein; osteoprotegerin; OPG; Fc protein; osteopathic;  
 XX therapy; bone loss; osteoporosis; Paget's disease; osteomyelitis;  
 KW hypercalcaemia; osteopenia; osteonecrosis; rheumatoid arthritis;  
 KW osteolytic metastasis; prosthetic loosening; immunoglobulin G1; IgG1;  
 KW periodontal.  
 XX Homo sapiens.  
 OS WO200118203-A1.  
 XX 15-MAR-2001.  
 PD 18-AUG-2000; 2000WO-US022797.  
 XX 03-SEP-1999; 99US-00389782.  
 XX (AMGE-) AMGEN INC.  
 PA

Dunstan CR, Wooden SK, Mann MB;  
 WPI; 2001-244572/25.  
 Osteoprotegerin-Fc protein fusions useful for treating bone loss caused by e.g. osteoporosis, Paget's disease and osteomyelitis.  
 Claim 3; Fig 1; 119pp; English.  
 The patent discloses fusion protein comprising human osteoprotegerin (OPG) protein fused by linker to human IgG1 Fc portion. OPG negatively regulates formation of osteoclasts in vitro and in vivo. It blocks the differentiation of osteoclasts from monocyte or macrophage precursors and the reabsorption of bone. The OPG-Fc fusion protein is administered for the treatment of bone loss resulting from osteoporosis, Paget's disease, osteomyelitis, hypercalcaemia, osteopenia associated with surgery or steroid administration, osteonecrosis, bone loss due to rheumatoid arthritis, periodontal bone loss, osteolytic metastasis and/or prosthetic loosening. The present sequence is partial human immunoglobulin G (Ig G) 1 protein comprising the hinge and heavy chain constant regions CH2 and CH3  
 Sequence 232 AA;  
 Query Match 97.2%; Score 1225; DB 4; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 1.6e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVHLQDMNGKEYCKVSNKALPAPIEKT 120  
 61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVHLQDMNGKEYCKVSNKALPAPIEKT 120  
 121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 121 ISKAGQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 181 PVLDSVGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232  
 181 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232

## RESULT 8

AE15347

AAE15347 standard; protein; 232 AA.

AAE15347;

09-APR-2002 (first entry)

Human immunoglobulin G (IgG) gamma 1 constant heavy chain hinge region.

Human; erythropoietin; Epo; haematocrit; anaemia; kidney function; IgG; cancer; myelosuppressive therapy; anti-viral drug; immunoglobulin G.

Homo sapiens.

WO200181405-A2.

01-NOV-2001.

19-APR-2001; 2001WO-US012836.

21-APR-2000; 2000US-00559001.

(AMGE-) AMGEN INC.

Egrie JC, Elliott SG, Browne JK, Sitney KC;

WPI; 2002-034433/04.

Increasing and maintaining hematocrit in mammal suffering from anemia, comprising administering hyperglycosylated analog of erythropoietin less frequently and at lower molar amount of recombinant human erythropoietin.

Example 1; Fig 10; 95pp; English.

The invention relates to a method for increasing and maintaining haematocrit in a mammal. The method comprises administering a hyperglycosylated analogue of erythropoietin (Epo) in a pharmaceutical composition, less frequently than an equivalent molar amount of and at a lower molar amount than recombinant human Epo (rHuEpo) to obtain a comparable target haematocrit. Epo is a glycoprotein hormone necessary for the maturation of erythroid progenitor cells into erythrocytes. Human Epo analogue is useful for raising and maintaining haematocrit to a comparable target haematocrit in a mammal suffering from anaemia associated with a decline or loss of kidney function, myelosuppressive therapy comprising chemotherapeutic or anti-viral drugs or associated with excessive blood loss during surgical procedures, and in cancer condition. The present sequence is human immunoglobulin G (IgG) gamma 1 constant heavy chain (CH2, CH3) hinge region used to construct Epo hyperglycosylated analogue fusion protein

Sequence 232 AA;

Query Match 97.2%; Score 1225; DB 5; Length 232;

Best Local Similarity 97.0%; Pred. No. 1.6e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60

61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVHLQDMNGKEYCKVSNKALPAPIEKT 120

61 NWYVDGVEVHNKTPREEQYNSTYRVVSVLTVHLQDMNGKEYCKVSNKALPAPIEKT 120

121 ISKAVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180

121 ISKAGQPREPOVYTLPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180

181 PVLDSVGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232

181 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232

## RESULT 9

AAE26272

AAE26272 standard; protein; 232 AA.

AAE26272;

14-NOV-2002 (first entry)

Human IgG1 heavy chain.

Human; amyloidogenic protein; Alzheimer's disease; Huntington's disease; spongiform encephalopathy; familial amyloid cardiomyopathy; amyloidosis; Gerstmann-Strausler-Scheinker syndrome; spongiform encephalopathy; GSS; Creutzfeldt-Jacob disease; insulinoma; diabetes; body myocytis; myeloma; CJ.

Homo sapiens.

WO200242462-A2.

30-MAY-2002.

27-NOV-2001; 2001WO-US044581.

27-NOV-2000; 2000US-0253302P.

29-NOV-2000; 2000US-0250198P.

PR 20-DEC-2000; 2000US-0257186P.  
 XX (PRAE-) PRAECIS PHARM INC.  
 XX  
 XX Geffer ML, Israel DI, Joyal JL, Gosselin M;  
 XX WPI; 2002-636427/68.  
 XX  
 XX Novel therapeutic agent useful for treating an amyloidogenic disorder,  
 PT e.g. Alzheimer's disease, comprises an immunoglobulin heavy chain  
 PT constant region linked to a peptide capable of binding amyloidogenic  
 PT protein.  
 XX  
 XX Example 8; Page 76; 79pp; English.  
 XX  
 CC The invention relates to a compound comprising an immunoglobulin (Ig)  
 CC heavy chain constant region or its fragment that retains the ability to  
 CC bind an Fc receptor linked by a linker group or a direct bond to a  
 CC peptide capable of binding an amyloidogenic protein. The invention is  
 CC useful for clearing an amyloidogenic protein such as beta-amyloid,  
 CC transthyretin (TTR), prion protein (PrP), islet amyloid polypeptide  
 CC (IAPP), atrial natriuretic factor (ANF), kappa light chain, lambda light  
 CC chain, amyloid A, procalcitonin, cystatin C, beta2-microglobulin, ApoA-I,  
 CC gelsolin, calcitonin, fibrinogen, Huntingtin, alpha-synuclein and  
 CC lysozyme from a subject and for treating an amyloidogenic disorder such  
 CC as Alzheimer's disease and spongiform encephalopathy. Disorders treatable  
 CC include those caused or characterised by deposits of TTR (eg. familial  
 CC amyloid cardiomyopathy), PrP (eg. spongiform encephalopathies, including  
 CC scrapie in sheep, bovine spongiform encephalopathy in cows and  
 CC Creutzfeldt-Jacob disease (CJ) and Gerstmann-Strausler-Scheinker  
 CC syndrome (GSS) in humans), IAPP (eg. insulinoma, adult onset diabetes),  
 CC ANF (eg. isolated atrial amyloid), kappa or lambda light chain (eg.  
 CC idiopathic amyloidosis, myeloma), amyloid A (eg. amyloidosis), Apo A-I  
 CC (eg. hereditary non-neuropathic systemic amyloidosis), Gelsolin (eg.  
 CC familial amyloidosis of Finnish type), Fibrinogen (eg. hereditary renal  
 CC amyloidosis), lysozyme (eg. hereditary systemic amyloidosis). Other  
 CC examples of amyloidogenic disorders include Huntington's disease and  
 CC inclusion body myocytis. The present sequence is human IgG1 heavy chain,  
 CC used in the exemplification of the invention  
 XX  
 SQ Sequence 232 AA;  
 Query Match 97.2%; Score 1225; DB 5; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 1.6e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCPPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 DB 1 EPKSCDKTHTCPPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 QY 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTCLVKGFYPSDIAVEWESNGQPENNYKTP 120  
 DB 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTCLVKGFYPSDIAVEWESNGQPENNYKTP 120  
 QY 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 DB 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232  
 DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232  
 RESULT 10  
 ADJ65991  
 ID ADJ65991 standard; protein; 232 AA.  
 XX  
 XX AC ADJ65991;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 XX Herpes virus entry mediator-related protein #2.  
 DE  
 XX

KW therapeutic agent; endotoxin induced disease; fusion protein;  
 KW Herpes virus entry mediator; HVEM; immunoglobulin Fc domain;  
 XX endotoxin shock; human.  
 XX Homo sapiens.  
 XX JP2003128576-A.  
 XX 08-MAY-2003.  
 XX 25-OCT-2001; 2001JP-00328430.  
 XX 25-OCT-2001; 2001JP-00328430.  
 XX (TAIS ) TAISHO PHARM CO LTD.  
 XX (GENE-) GENE TECHNO SCI KK.  
 XX WPI; 2003-817833/77.  
 XX N-PSDB; ADJ65998.  
 PT New therapeutic agent, useful for treating endotoxin induced disease,  
 PT comprises fusion protein of Herpes virus entry mediator protein and  
 PT immunoglobulin.  
 XX  
 CC Claim 5; SEQ ID NO 2; 11pp; Japanese.  
 CC The invention comprises a therapeutic agent for treating endotoxin  
 CC induced disease, the therapeutic agent contains a fusion protein of the  
 CC Herpes virus entry mediator (HVEM) protein and an immunoglobulin Fc  
 CC domain. The therapeutic agent of the invention is useful for treating  
 CC endotoxin induced disease, such as endotoxin shock. The present amino  
 CC acid sequence represents a human protein which is claimed in the  
 CC specification.  
 XX  
 SQ Sequence 232 AA;  
 Query Match 97.2%; Score 1225; DB 7; Length 232;  
 Best Local Similarity 97.0%; Pred. No. 1.6e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
 QY 1 EPKSCDKTHTCPPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 DB 1 EPKSCDKTHTCPPAPPELLGGPSVFLPFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 QY 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTCLVKGFYPSDIAVEWESNGQPENNYKTP 120  
 DB 61 NWYVDGVEVHNKTKPREEQNSTYRVVSVLTCLVKGFYPSDIAVEWESNGQPENNYKTP 120  
 QY 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 DB 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232  
 DB 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYQOQSLSLSPGK 232  
 RESULT 11  
 ADJ57512  
 ID ADJ57512 standard; protein; 232 AA.  
 XX  
 XX AC ADJ57512;  
 XX  
 DT 06-MAY-2004 (first entry)  
 XX  
 XX Human IgG1 Fc domain fragment.  
 XX  
 XX TF; tissue factor; FVIIa; factor VII; anticoagulant; thrombolytic;  
 XX cerebroprotective; cytotatic; vasotrophic; antirheumatic; antiarthritic;  
 XX antiarteriosclerotic; antiinflammatory; antibacterial; immunosuppressive;  
 XX hypertensive; cardiac; coagulation factor VII; human; immunoglobulin G1;  
 XX IgG1.  
 XX

3 Homo sapiens.  
4 WO2004006962-A2.  
5 22-JAN-2004.  
6 09-JUL-2003; 2003WO-DK000481.  
7 12-JUL-2002; 2002DK-00001099.  
8 (NOVO ) NOVO NORDISK AS.  
9 Bjorn SE, Nicolaisen EM, Steenstrup TD;  
10 WPI; 2004-180224/17.  
11 New compound binding to tissue factor, useful for treating diseases such  
12 as angiogenesis, ischemia/reperfusion, and rheumatoid arthritis.  
13 Claim 15; SEQ ID NO 7; 51pp; English.  
14 The invention relates to a compound (I) binding to tissue factor (TF).  
15 The compound (I) has the formula A-(LM)-C, where A is a FVIIa  
16 polypeptide, LM is an optional linker group, C comprises an  
17 immunostimulatory effector domain, and (I) binds to TF. (I) inhibits TF-  
18 mediated activated factor VII (FVIIa) activity. (I) is useful as a  
19 medicament, and for the manufacture of a medicament for preventing or  
20 treating disease or disorder associated with pathophysiological TF  
21 activity. The disease or disorder associated with pathophysiological TF  
22 activity are deep venous thrombosis, arterial thrombosis, post surgical  
23 thrombosis, coronary artery bypass graft (CABG), percutaneous transluminal  
24 coronary angioplasty (PTCA), stroke, cancer, tumor metastasis,  
25 angiogenesis, ischemia/reperfusion, rheumatoid arthritis, thrombolysis,  
26 arteriosclerosis and restenosis following angioplasty, acute and chronic  
27 indications such as inflammation, septic shock, septicemia, hypotension,  
28 adult respiratory distress syndrome (ARDS), disseminated intravascular  
29 coagulopathy (DIC), pulmonary embolism, platelet deposition, myocardial  
30 infarction, or prophylactic treatment of mammals with atherosclerotic  
31 vessels at risk for thrombosis. The present sequence represents the Fc  
32 domain fragment of human immunoglobulin G1 (IgG1).  
33 Sequence 232 AA;  
34 Query Match 97.2%; Score 1225; DB 8; Length 232;  
35 Best Local Similarity 97.0%; Pred. No. 1.6e-88;  
36 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
37 Y 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
38 b 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
39 Y 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKVSKNKPAPIEKT 120  
40 b 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKVSKNKPAPIEKT 120  
41 Y 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
42 b 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
43 Y 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVPCSWMEALHNHYQOQSLSLSPGK 232  
44 b 181 PVLDSGGSFFLYSKLTVDKSRWQQGNVPCSWMEALHNHYQOQSLSLSPGK 232  
45 RESULT 12  
46 BB09463  
47 D ABB09463 standard; protein; 233 AA.  
48 C ABB09463;  
49 X 01-JUL-2002 (first entry)  
50 T Human IgG Fc fragment amino acid sequence.  
51 E

XX Protein A; immunoglobulin G; IgG; antibody; human.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
XX PH Misc-difference 168  
XX FT /note= "encoded by GAC"  
XX FT Misc-difference 169  
XX FT /note= "encoded by ACC"  
XX W0200204602-A1.  
XX 17-JAN-2002.  
XX 04-JUL-2001; 2001WO-JP005798.  
XX 07-JUL-2000; 2000JP-00206689.  
XX (GENC-) GENCOM CORP.  
XX Tanaka A, Ueda M, Teranishi Y;  
XX WPI; 2002-148174/19.  
XX N-PSDB; ABL52834.  
XX Transformant yeast for stable supply of highly active catalytic antibody,  
XX comprises the capability of expressing and presenting protein A or its  
XX fragment, particularly with the ZZ domain, on the cell surface.  
XX Example 3; Fig 4; 25pp; Japanese.  
XX The invention relates to a transformant yeast that can present protein A  
XX or its fragment on its cell surface. The yeast can be used for detecting  
XX or isolating the Fc part of immunoglobulin (Ig)G. The yeast is useful for  
XX a stable supply of highly active catalytic antibody e.g. by screening  
XX novel functional molecules and in isolating Fc-carrying secretory  
XX proteins. The yeast of the invention is capable of adhering specifically  
XX to a combinatorial antibody library with an Fc-carrying antibody  
XX component. The current sequence represents the human IgG Fc fragment  
XX amino acid sequence  
XX Sequence 233 AA;  
XX Query Match 97.2%; Score 1225; DB 5; Length 233;  
XX Best Local Similarity 97.0%; Pred. No. 1.6e-88;  
XX Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
XX QY 1 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
XX Db 2 EPKSCDKHTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 61  
XX QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKVSKNKPAPIEKT 120  
XX Db 62 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQNWMMGKEYCKVSKNKPAPIEKT 121  
XX QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
XX Db 122 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 181  
XX QY 181 PVLDSVGSFFLYSKLTVDKSRWQQGNVPCSWMEALHNHYQOQSLSLSPGK 232  
XX Db 182 PVLDSGGSFFLYSKLTVDKSRWQQGNVPCSWMEALHNHYQOQSLSLSPGK 233  
XX RESULT 13  
XX ABJ38647  
XX ID ABJ38647 standard; protein; 235 AA.  
XX AC ABJ38647;  
XX X 26-JUN-2003 (first entry)  
XX DT Human IgG Fc fragment amino acid sequence.  
XX E

PCXFC protein SEQ ID No 6.

Cytostatic; osteopathic; cerebroprotective; dermatological; enzyme; antigen binding; receptor protein tyrosine kinase; skeletal dysplasia; constitutive activation; craniostenosis; cell proliferative disorder; achondroplasia; thanatophoric dysplasia; acanthosis nigricans dysplasia; hypochondroplasia; severe achondroplasia; transitional cell carcinoma; Muenke coronal craniostenosis; Crouzon syndrome; acanthosis nigricans; tumour progression; osteosarcoma; chondrosarcoma; multiple myeloma; mammary carcinoma; fibroblast growth factor receptor 3; FGFR3 protein.

Homo sapiens.

WO2002102854-A2.

27-DEC-2002.

20-JUN-2002; 2002MO-IB003523.

20-JUN-2001; 2001US-0299187P.

(MORP-) MORPHOSYS AG.

(PROC-) PROCHON BIOTECH LTD.

Thomassen-Wolf E, Borges E, Yayon A, Rom E;

WPI; 2003-167489/16.

N-PSDB; ABT40262.

New molecules having the antigen-binding portion of antibodies that block activation of receptor protein tyrosine kinase, useful for treating or inhibiting skeletal dysplasias, craniostenosis or cell proliferative disorders.

Example 2; Page 38; 103pp; English.

The invention relates to a novel molecule comprising the antigen binding portion of an isolated antibody, which has an increased affinity for a receptor protein tyrosine kinase and which blocks constitutive activation of the receptor protein tyrosine kinase. The methods and compositions of the invention are useful for treating or inhibiting a skeletal dysplasia, craniostenosis or a cell proliferative disorder. The skeletal dysplasia is achondroplasia, thanatophoric dysplasia, hypochondroplasia, severe achondroplasia with developmental delay or acanthosis nigricans dysplasia. The craniostenosis disorder is Muenke coronal craniostenosis or Crouzon syndrome with acanthosis nigricans. The cell proliferative disorder is tumour progression that is progression of transitional cell carcinoma, osteosarcoma, chondrosarcoma, multiple myeloma or mammary carcinoma. This sequence represents a protein derived from a PCXFC plasmid DNA vector relating to the protein tyrosine kinase inhibitor of the invention

Sequence 235 AA;

Query Match

Best Local Similarity 97.2%; Score 1225; DB 6; Length 235;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKCDKTHTPCPAPLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Db 4 EPKCDKTHTPCPAPLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 63

QY 61 NWYDGVGVHNVKTPREEQVNSTYRVSVTLVHQNMMNGKYEKCKVSNKALPAPIETK 120

Db 64 NWYDGVGVHNAKTPREEQVNSTYRVSVTLVHQNMMNGKYEKCKVSNKALPAPIETK 123

QY 121 ISKAKQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180

Db 124 ISKAKQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 183

QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYQORSLSLSPGK 232

Db 184 PVLDSGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYQORSLSLSPGK 235

RESULT 14

ADA89055

ID ADA89055 standard; protein; 235 AA.

XX AC ADA89055;

XX DT 20-NOV-2003 (first entry)

XX DE Plasmid pCXFc amino acid sequence SEQ ID NO:6.

XX KW antigen binding; antibody; specific binding affinity;

XX KW receptor protein tyrosine kinase; RPTK;

XX KW receptor protein tyrosine kinase inhibitor;

XX KW fibroblast growth factor receptor; FGFR; osteopathic; cytostatic;

XX KW ophthalmological; bone disorder; cartilage disorder; skeletal disorder;

XX KW skeletal dysplasia; achondroplasia; thanatophoric dysplasia;

XX KW hypochondroplasia; craniostenosis disorder;

XX KW malignant cell proliferative disease; cancer; tumour; vision disorder;

XX KW non-neoplastic angiogenic pathologic condition.

XX OS Synthetic.

OS Homo sapiens.

XX WO2002102973-A2.

XX PD 27-DEC-2002.

XX PF 20-JUN-2002; 2002MO-IL000495.

XX PR 20-JUN-2001; 2001US-0299187P.

XX PA (PROC-) PROCHON BIOTECH LTD.

XX PI Yayon A, Rom E;

XX WPI; 2003-175236/17.

DR N-PSDB; ADA89054.

XX New antibodies which have specific binding affinity for a receptor protein tyrosine kinase (RPTK) and block constitutive activation of RPTK, useful for treating bone and cartilage disorders, or malignant cell proliferative diseases.

Example 2; Page 43; 122pp; English.

The present invention describes a molecule (I) comprising the antigen binding portion of an isolated antibody which has specific binding affinity for a receptor protein tyrosine kinase (RPTK), particularly for a fibroblast growth factor receptor (FGFR), and which blocks constitutive activation of an RPTK. Also described: (1) pharmaceutical compositions comprising (I) as an active ingredient and a pharmaceutical carrier, excipient, or auxiliary agent; (2) a kit comprising (I), at least one reagent for detecting the presence of (I) when bound to the RPTK, and instructions for use; (3) a method for treatment of bone and cartilage related disorders by administering a composition of (I) to the subject; (4) a method for treating or inhibiting a cell proliferative disease or disorder by administering the composition of (I); (5) a method for screening a molecule comprising the antigen-binding portion of an antibody which blocks ligand-dependent activation of RPTK; (6) an isolated nucleic acid molecule encoding a VI-CDR3 DNA region and a VH-CDR3 DNA region; (7) an isolated nucleic acid molecule encoding VI region and a VH region; (8) vectors comprising a nucleic acid molecule of (6) or (7); and (9) host cells transformed with the vector. (I) have osteopathic, cytostatic and ophthalmological activities, and can be used as a RPTK inhibitor. Compositions comprising (I) are useful for treating bone and cartilage disorders, including skeletal disorders such as skeletal dysplasia (achondroplasia, thanatophoric dysplasia, hypochondroplasia, severe achondroplasia with developmental delay and acanthosis nigricans dysplasia) or a craniostenosis disorder (e.g. Muenke coronal craniostenosis or Crouzon syndrome with acanthosis nigricans). The composition may also be used for treating or inhibiting

malignant cell proliferative disease or disorder associated with abnormal RPTK activity, including a haematopoietic malignancy (e.g. multiple myeloma), solid tumours (e.g. mammary, colon, cervical, bladder, colorectal, chondrosarcoma or osteosarcoma), tumour formation, primary tumours, tumour progression (particularly progression of transitional cell carcinoma or mammary carcinoma), or tumour metastasis, where the cell proliferative disorder may be associated with the action of a constitutively activated RPTK, or with ligand-dependent activation of RPTK. The compositions may further be used for treating hyperproliferative diseases and disorders associated with ligand-dependent EGFR signaling, such as vision disorders (e.g. neovascular glaucoma, macular degeneration and proliferative retinopathy including diabetic retinopathy), and non-neoplastic angiogenic pathologic conditions (e.g. haemangiomas, angiofibromas and psoriasis). The present sequence is given in the exemplification of the present invention.

Sequence 235 AA;

Query Match 97.2%; Score 1225; DB 6; Length 235;  
 Best Local Similarity 97.0%; Pred. No. 1.6e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 4 EPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 63  
 61 NWYDGVVHNVKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120  
 64 NWYDGVVHNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 123  
 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 124 ISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 183  
 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYHQBSLSLSPGK 232  
 184 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYHQBSLSLSPGK 235

3525647  
 ADD25647 standard; protein; 235 AA.  
 ADD25647;  
 15-JAN-2004 (first entry)  
 Binding domain-immunoglobulin fusion protein-associated protein #101.  
 Binding domain; immunoglobulin; fusion protein; cytotaxtic;  
 antiarthritic; immunosuppressive; antidiabetic; antithyroid;  
 neuroprotective; hinge region; immunoglobulin heavy chain;  
 CH2 constant region; CH3 constant region; IgG1;  
 antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;  
 malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma;  
 rheumatoid arthritis; myasthenia gravis; Grave's disease;  
 type I diabetes mellitus; multiple sclerosis; autoimmune disease.

Unidentified.  
 US2003118592-A1.  
 26-JUN-2003.  
 25-JUL-2002; 2002US-00207655.  
 17-JAN-2001; 2001US-0367358P.  
 17-JAN-2002; 2002US-00053530.  
 03-JUN-2002; 2002US-0385691P.  
 (GENE-) GENE-CRAFT INC.  
 Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

XX WPI; 2003-801317/75.  
 DR New binding domain-immunoglobulin fusion protein, useful for treating a  
 XX subject having or suspected of having a malignant condition or a B-cell  
 PT disorder, e.g. melanoma, Grave's disease or autoimmune disease.  
 XX Disclosure; SEQ ID NO 208; 157pp; English.  
 PS The invention relates to a binding domain-immunoglobulin fusion protein  
 CC comprising a binding domain polypeptide that is fused to an  
 CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain  
 CC CH2 constant region polypeptide that is fused to the hinge region  
 CC polypeptide, and an immunoglobulin heavy chain CH3 constant region  
 CC polypeptide that is fused to the CH2 constant region polypeptide. The  
 CC hinge region polypeptide comprises a wild-type human IgG1 immunoglobulin  
 CC hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge  
 CC region polypeptide; derived from (a) having 3 or more cysteine residues;  
 CC where the mutated human IgG1 immunoglobulin hinge region polypeptide  
 CC contains 2 cysteine residues, where the first cysteine is not mutated; a  
 CC mutated human IgG1 immunoglobulin hinge region polypeptide, derived from  
 CC (a) having 3 or more cysteine residues, where the mutated human IgG1  
 CC immunoglobulin hinge region polypeptide contains no more than one  
 CC cysteine residue; and a mutated human IgG1 immunoglobulin hinge  
 CC polypeptide, derived from (a) having 3 or more cysteine residues; where  
 CC the mutated human IgG1 immunoglobulin hinge region polypeptide contains  
 CC no cysteine residues. The binding domain-immunoglobulin fusion protein is  
 CC capable of at least one immunological activity comprising antibody  
 CC dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The  
 CC binding domain polypeptide is capable of specifically binding to an  
 CC antigen. Also included are an isolated polynucleotide encoding the  
 CC binding domain-immunoglobulin fusion protein, a recombinant expression  
 CC construct comprising the polynucleotide (operably linked to a promoter),  
 CC a host cell transformed or transfected with a recombinant expression  
 CC construct, producing the binding domain-immunoglobulin fusion protein, a  
 CC pharmaceutical composition comprising the binding domain-immunoglobulin  
 CC fusion protein or polynucleotide and a carrier, and treating a subject  
 CC having or suspected of having a malignant condition or a B-cell disorder.  
 CC The binding domain-immunoglobulin fusion protein is useful for treating a  
 CC subject having or suspected of having a malignant condition or a B-cell  
 CC disorder, e.g. melanoma, carcinoma or sarcoma, rheumatoid arthritis,  
 CC myasthenia gravis, Grave's disease, type I diabetes mellitus, multiple  
 CC sclerosis or autoimmune disease. The present sequence is a binding domain  
 CC -immunoglobulin fusion protein-associated protein sequence. Note: The  
 CC sequence data for this patent formed part of the printed specification  
 CC and is also available in electronic format directly from USPTO at  
 CC seqdata.uspto.gov/sequence.html?DocID=20030118592. The authors have not  
 CC identified the sequences in the printed specification by their SEQ ID  
 CC number therefore none of the sequences can be explicitly identified.  
 XX Sequence 235 AA;

Query Match 97.2%; Score 1225; DB 7; Length 235;  
 Best Local Similarity 97.0%; Pred. No. 1.6e-88;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
 4 EPKSCDKTHTCPCPAPPELLGGPSVFLPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 63  
 61 NWYDGVVHNVKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 120  
 64 NWYDGVVHNAKTPREBQYNSTYRVVSVLTVLHQDWLNGKEYKCKVSNKALPAPIEKT 123  
 121 ISKAKVQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
 124 ISKAKQPREPOVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 183  
 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYHQBSLSLSPGK 232  
 184 PVLDSGSGFFLYSKLTVDKSRWQGNVFCSCVMHEALHNYHQBSLSLSPGK 235

Ledbetter JA, Hayden-Ledbetter MS, Thompson PA;

Search completed: October 27, 2004, 16:59:37  
Job time : 91.7544 secs



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Copyright (c) 1993 - 2004 Compugen Ltd.  
1 protein - protein search, using sw model  
in on: October 27, 2004, 17:04:05 ; Search time 71.0036 Seconds  
(without alignments)  
1059.356 Million cell updates/sec

US-10-000-439-3  
Perfect score: 1260  
Sequence: 1 EPKSCDKTHTCPPCPAPPELL.....MHEALHHYQORSLSLSPGK 232

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

searched: 1370721 seqs, 324215800 residues

total number of hits satisfying chosen parameters: 1370721

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Fast-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:\*

- 1: /cgn2\_6/ptodata/1/pubaa/US07\_PUBCOMB.pep.\*
- 2: /cgn2\_6/ptodata/1/pubaa/PCT\_NEW\_PUB.pep.\*
- 3: /cgn2\_6/ptodata/1/pubaa/US06\_NEW\_PUB.pep.\*
- 4: /cgn2\_6/ptodata/1/pubaa/US06\_PUBCOMB.pep.\*
- 5: /cgn2\_6/ptodata/1/pubaa/US07\_NEW\_PUB.pep.\*
- 6: /cgn2\_6/ptodata/1/pubaa/PCTUS\_PUBCOMB.pep.\*
- 7: /cgn2\_6/ptodata/1/pubaa/US08\_NEW\_PUB.pep.\*
- 8: /cgn2\_6/ptodata/1/pubaa/US08\_PUBCOMB.pep.\*
- 9: /cgn2\_6/ptodata/1/pubaa/US09A\_PUBCOMB.pep.\*
- 10: /cgn2\_6/ptodata/1/pubaa/US09B\_PUBCOMB.pep.\*
- 11: /cgn2\_6/ptodata/1/pubaa/US09C\_PUBCOMB.pep.\*
- 12: /cgn2\_6/ptodata/1/pubaa/US09\_NEW\_PUB.pep.\*
- 13: /cgn2\_6/ptodata/1/pubaa/US10A\_PUBCOMB.pep.\*
- 14: /cgn2\_6/ptodata/1/pubaa/US10B\_PUBCOMB.pep.\*
- 15: /cgn2\_6/ptodata/1/pubaa/US10C\_PUBCOMB.pep.\*
- 16: /cgn2\_6/ptodata/1/pubaa/US10D\_PUBCOMB.pep.\*
- 17: /cgn2\_6/ptodata/1/pubaa/US10\_NEW\_PUB.pep.\*
- 18: /cgn2\_6/ptodata/1/pubaa/US11\_NEW\_PUB.pep.\*
- 19: /cgn2\_6/ptodata/1/pubaa/US60\_NEW\_PUB.pep.\*
- 20: /cgn2\_6/ptodata/1/pubaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1260	100.0	232	10	US-09-847-208-3
2	1260	100.0	232	14	US-10-000-439-3
3	1260	100.0	330	10	US-09-847-208-2
4	1260	100.0	330	14	US-10-000-439-2
5	1260	100.0	569	10	US-09-847-208-7
6	1260	100.0	569	14	US-10-000-439-7
7	1225	97.2	232	9	US-09-996-357-10
8	1225	97.2	232	10	US-09-389-782-1
9	1225	97.2	232	16	US-10-761-619-7
10	1225	97.2	232	16	US-10-761-593A-26
11	1225	97.2	235	14	US-10-207-655-208
12	1225	97.2	247	9	US-09-996-357-13
13	1225	97.2	251	14	US-10-008-063-18

14	1225	97.2	251	14	US-10-152-363A-6	Sequence 6, Appli
15	1225	97.2	267	9	US-09-996-357-12	Sequence 12, Appl
16	1225	97.2	288	10	US-09-822-851B-14	Sequence 14, Appl
17	1225	97.2	288	14	US-10-119-637A-14	Sequence 14, Appl
18	1225	97.2	329	15	US-10-370-749-48	Sequence 48, Appl
19	1225	97.2	330	10	US-09-995-898A-15	Sequence 15, Appl
20	1225	97.2	330	10	US-09-892-949-38	Sequence 38, Appl
21	1225	97.2	330	13	US-10-047-542-20	Sequence 20, Appl
22	1225	97.2	330	14	US-10-269-805-68	Sequence 68, Appl
23	1225	97.2	330	14	US-10-310-713-8	Sequence 8, Appl
24	1225	97.2	330	14	US-10-112-582-1	Sequence 1, Appli
25	1225	97.2	330	14	US-10-320-231A-81	Sequence 81, Appl
26	1225	97.2	330	14	US-10-383-902A-6	Sequence 6, Appli
27	1225	97.2	330	15	US-10-408-901-2	Sequence 2, Appli
28	1225	97.2	330	15	US-10-420-034A-15	Sequence 15, Appl
29	1225	97.2	330	15	US-10-257-907-5	Sequence 5, Appli
30	1225	97.2	330	15	US-10-656-769-2	Sequence 2, Appli
31	1225	97.2	330	16	US-10-679-620-58	Sequence 58, Appl
32	1225	97.2	330	16	US-10-772-531-38	Sequence 38, Appl
33	1225	97.2	330	17	US-10-479-326-1	Sequence 1, Appli
34	1225	97.2	331	9	US-09-761-413-2	Sequence 2, Appli
35	1225	97.2	331	14	US-10-341-836-2	Sequence 2, Appli
36	1225	97.2	332	10	US-09-990-586-98	Sequence 98, Appl
37	1225	97.2	332	14	US-10-310-113-167	Sequence 167, App
38	1225	97.2	332	14	US-10-230-880-98	Sequence 98, Appl
39	1225	97.2	333	15	US-10-272-899A-8	Sequence 8, Appli
40	1225	97.2	356	15	US-10-372-899A-72	Sequence 72, Appl
41	1225	97.2	358	14	US-10-233-150-5	Sequence 5, Appli
42	1225	97.2	360	9	US-09-949-713-11	Sequence 11, Appl
43	1225	97.2	367	15	US-10-452-646-9	Sequence 9, Appli
44	1225	97.2	371	14	US-10-157-408-7	Sequence 7, Appli
45	1225	97.2	371	14	US-10-097-044A-7	Sequence 7, Appli

ALIGNMENTS

RESULT 1  
US-09-847-208-3  
; Sequence 3, Application US/09847208  
; Publication No. US20030082190A1  
; GENERAL INFORMATION:  
; APPLICANT: Saxon, Andrew  
; APPLICANT: Zhang, Xe  
; APPLICANT: Zhu, Daosheng  
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF  
; FILE REFERENCE: UG57.002A  
; CURRENT APPLICATION NUMBER: US/09/847,208  
; CURRENT FILING DATE: 2001-05-01  
; NUMBER OF SEQ ID NOS: 177  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 3  
; LENGTH: 232  
; TYPE: PRT  
; ORGANISM: Homo sapiens  
US-09-847-208-3

Query Match	100.0%	Score 1260;	DB 10;	Length 232;
Best Local Similarity	100.0%	Pred. NO. 9.8e-93;		
Matches 232;	Conservative	0;	Mismatches 0;	Indels 0;
Gaps	0;			
QY	1	EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF	60	
DB	1	EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF	60	
QY	61	NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVTLQHWMMNGKEYCKVKCNKALPAPEKT	120	
DB	61	NNYVDGVEVHNKTKPREEQYNSTYRVVSVLTVTLQHWMMNGKEYCKVKCNKALPAPEKT	120	
QY	121	ISKAKVQPREQVQVTLPPSRDELTKNOVSLTCLVKGYPSDIAVENESNGQPNNYKTP	180	
DB	121	ISKAKVQPREQVQVTLPPSRDELTKNOVSLTCLVKGYPSDIAVENESNGQPNNYKTP	180	

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QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYQORSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYQORSLSLSPGK 232

RESULT 2
US-10-000-439-3
; Sequence 2, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; FILE REFERENCE: UC67.004A
; CURRENT FILING DATE: 2001-10-24
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 3
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-3

Query Match 100.0%; Score 1260; DB 14; Length 232;
Best Local Similarity 100.0%; Pred. No. 9.8e-93;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKVSKNKPAPIEKT 120
DB 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKVSKNKPAPIEKT 120
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYQORSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYQORSLSLSPGK 232

RESULT 3
US-09-847-208-2
; Sequence 2, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daoheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; FILE REFERENCE: UC67.002A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-847-208-2

Query Match 100.0%; Score 1260; DB 10; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.5e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKVSKNKPAPIEKT 120
DB 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKVSKNKPAPIEKT 120
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 180
DB 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 180
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYQORSLSLSPGK 232
DB 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYQORSLSLSPGK 232

RESULT 4
US-10-000-439-2
; Sequence 2, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; FILE REFERENCE: UC67.004A
; CURRENT FILING DATE: 2001-10-24
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-2

Query Match 100.0%; Score 1260; DB 14; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.5e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKVSKNKPAPIEKT 120
DB 159 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKVSKNKPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYQORSLSLSPGK 232
DB 279 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYQORSLSLSPGK 330

RESULT 5
US-09-847-208-7
; Sequence 7, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daoheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; FILE REFERENCE: UC67.002A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
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QY 1 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
DB 99 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKVSKNKPAPIEKT 120
DB 159 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKVSKNKPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYQORSLSLSPGK 232
DB 279 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYQORSLSLSPGK 330

RESULT 4
US-10-000-439-2
; Sequence 2, Application US/10000439
; Publication No. US20030064063A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR
; FILE REFERENCE: UC67.004A
; CURRENT FILING DATE: 2001-10-24
; PRIOR FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 330
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-000-439-2

Query Match 100.0%; Score 1260; DB 14; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.5e-92;
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 99 EPKSCDKTHTCCPCPAPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 158
QY 61 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKVSKNKPAPIEKT 120
DB 159 NWYVDGVEVHNVTKPREEQYNSTYRVVSVLTVLHQNWNGKEYCKVSKNKPAPIEKT 218
QY 121 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 180
DB 219 ISKAKVQPREPOVYTLPPSRDELTKNOVSLTCLVKGFPYPSDIAVEWESNGQPENNYKTTTP 278
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYQORSLSLSPGK 232
DB 279 PVLDSVGSFFLYSKLTVDKSRWQGNVFSVMSHEALHNHYQORSLSLSPGK 330

RESULT 5
US-09-847-208-7
; Sequence 7, Application US/09847208
; Publication No. US20030082190A1
; GENERAL INFORMATION:
; APPLICANT: Saxon, Andrew
; APPLICANT: Zhang, Ke
; APPLICANT: Zhu, Daoheng
; TITLE OF INVENTION: FUSION MOLECULES AND TREATMENT OF
; FILE REFERENCE: UC67.002A
; CURRENT FILING DATE: 2001-05-01
; NUMBER OF SEQ ID NOS: 177
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SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 7

LENGTH: 569

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Fusion between hinge-CH2-CH3 (I9G1) to CH2-CH3-CH4  
OTHER INFORMATION: (I9E)

-09-847-208-7

Query Match 100.0%; Score 1260; DB 10; Length 569;  
Best Local Similarity 100.0%; Pred. No. 2.8e-92;  
Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120

61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120

121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180

121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180

181 PVLDVSGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYQORSLSLSPGK 232

181 PVLDVSGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYQORSLSLSPGK 232

SULT 6

1-10-000-439-7

Sequence 7, Application US/10000439

Publication No. US20030064063A1

GENERAL INFORMATION:

APPLICANT: Saxon, Andrew

TITLE OF INVENTION: FUSION MOLECULES AND METHODS FOR

TITLE OF INVENTION: TREATMENT OF IMMUNE DISEASES

FILE REFERENCE: UC067.004A

CURRENT APPLICATION NUMBER: US/10/000.439

CURRENT FILING DATE: 2001-10-24

PRIOR APPLICATION NUMBER: US 09/847,208

PRIOR FILING DATE: 2001-05-01

NUMBER OF SEQ ID NOS: 13

SOFTWARE: FastSeq for Windows Version 4.0

SEQ ID NO 7

LENGTH: 569

TYPE: PRT

ORGANISM: Unknown

FEATURE:

OTHER INFORMATION: Fusion polypeptide comprising a hinge-CH2-CH3

OTHER INFORMATION: (I9G1) sequence and a CH2-CH3-CH4 (I9E) sequence

1-10-000-439-7

Query Match

Best Local Similarity 100.0%; Score 1260; DB 14; Length 569;

Matches 232; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120

61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120

121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180

121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180

181 PVLDVSGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYQORSLSLSPGK 232

181 PVLDVSGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYQORSLSLSPGK 232

Db 181 PVLDVSGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYQORSLSLSPGK 232

RESULT 7

US-09-996-357-10

; Sequence 10, Application US/09996357

; Patent No. US20020133001A1

; GENERAL INFORMATION:

; APPLICANT: Gelfer, Malcolm L

; APPLICANT: Isreal, David I

; APPLICANT: Joval, John L

; APPLICANT: Gosselin, Michael

; TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR

; TITLE OF INVENTION: TREATING AN AMYLOIDOTIC DISEASE

; FILE REFERENCE: PEI-105

; CURRENT APPLICATION NUMBER: US/09/996,357

; CURRENT FILING DATE: 2001-11-27

; PRIOR APPLICATION NUMBER: 60/253,302

; PRIOR FILING DATE: 2000-11-27

; PRIOR APPLICATION NUMBER: 60/250,198

; PRIOR FILING DATE: 2000-11-29

; PRIOR APPLICATION NUMBER: 60/257,186

; PRIOR FILING DATE: 2000-12-20

; NUMBER OF SEQ ID NOS: 13

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 10

; LENGTH: 232

; TYPE: PRT

; ORGANISM: Homo sapiens

; US-09-996-357-10

Query Match 97.2%; Score 1225; DB 9; Length 232;

Best Local Similarity 97.0%; Pred. No. 6.1e-90;

Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

QY 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

Db 1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60

QY 61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120

Db 61 NWYVDGVEVHNKTKPREEQNSTYRVSVLTVLHQNMWNGKEYCKVSNKALPAPIEKT 120

QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180

Db 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180

QY 181 PVLDVSGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYQORSLSLSPGK 232

Db 181 PVLDVSGSFFLYSLKLTVDKSRWQGNVFCSCVMHEALHNHYQORSLSLSPGK 232

RESULT 8

US-09-389-782-1

; Sequence 1, Application US/09389782

; Publication No. US20030144187A1

; GENERAL INFORMATION:

; APPLICANT: Wooden, Scott K.

; APPLICANT: Mann, Michael B.

; APPLICANT: Dunstan, Colin R.

; TITLE OF INVENTION: OPG Fusion Protein Compositions and Methods

; FILE REFERENCE: A-604

; CURRENT APPLICATION NUMBER: US/09/389,782

; CURRENT FILING DATE: 1999-09-03

; NUMBER OF SEQ ID NOS: 50

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 232

; TYPE: PRT

; ORGANISM: Human

; US-09-389-782-1

Query Match 97.2%; Score 1225; DB 10; Length 232;

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; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
; FILE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-761-593A-26

Query Match          97.2%; Score 1225; DB 16; Length 232;
Best Local Similarity 97.0%; Pred. No. 6.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLTQHWMMNGKEKCKVSNKALPAPIKT 120
Db 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLTQHWMMNGKEKCKVSNKALPAPIKT 120
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Qy 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
Db 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232

RESULT 9
US-10-617-619-7
; Sequence 7, Application US/10617619
; Publication No. US20040110929A1
; GENERAL INFORMATION:
; APPLICANT: Bjorn, Soren E
; APPLICANT: Nicolaisen, Else M
; APPLICANT: Jorgensen, Anker S
; TITLE OF INVENTION: Tf Binding Compound
; FILE REFERENCE: 6455.200-US
; CURRENT APPLICATION NUMBER: US/10/617,619
; CURRENT FILING DATE: 2003-07-11
; PRIOR APPLICATION NUMBER: Danish Application No. PA 2002 01099
; PRIOR FILING DATE: 2002-07-12
; PRIOR APPLICATION NUMBER: US 60/404,568
; PRIOR FILING DATE: 2002-08-19
; NUMBER OF SEQ ID NOS: 13
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 7
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Human
US-10-617-619-7

Query Match          97.2%; Score 1225; DB 16; Length 232;
Best Local Similarity 97.0%; Pred. No. 6.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLTQHWMMNGKEKCKVSNKALPAPIKT 120
Db 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLTQHWMMNGKEKCKVSNKALPAPIKT 120
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Qy 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
Db 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232

RESULT 10
US-10-761-593A-26
; Sequence 26, Application US/10761593A
; Publication No. US20040175824A1
; GENERAL INFORMATION:
; APPLICANT: Sun, Lee-Hwei K
; APPLICANT: Sun, Bill N
; APPLICANT: Sun, Cecily R
```

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; TITLE OF INVENTION: Fc fusion proteins of human erythropoietin with high biological
; FILE OF INVENTION: activities
; FILE REFERENCE: 02SUN2001-A
; CURRENT APPLICATION NUMBER: US/10/761,593A
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 09/932812
; PRIOR FILING DATE: 2001-08-17
; NUMBER OF SEQ ID NOS: 28
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 26
; LENGTH: 232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-761-593A-26

Query Match          97.2%; Score 1225; DB 16; Length 232;
Best Local Similarity 97.0%; Pred. No. 6.1e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLTQHWMMNGKEKCKVSNKALPAPIKT 120
Db 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLTQHWMMNGKEKCKVSNKALPAPIKT 120
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 121 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Qy 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232
Db 181 PVLDSGSGFFLYSKLTVDKSRWQQGNVFCSCVMHEALHNHYTQKSLSLSPGK 232

RESULT 11
US-10-207-655-208
; Sequence 208, Application US/10207655
; Publication No. US20030118592A1
; GENERAL INFORMATION:
; APPLICANT: Ledbetter, Jeffrey A.
; APPLICANT: Hayden-Ledbetter, Martha S.
; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
; FILE REFERENCE: 390069.401C1
; CURRENT APPLICATION NUMBER: US/10/207,655
; CURRENT FILING DATE: 2002-07-25
; NUMBER OF SEQ ID NOS: 426
; SOFTWARE: Patent in version 3.0
; SEQ ID NO 208
; LENGTH: 235
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Fusion polypeptide
US-10-207-655-208

Query Match          97.2%; Score 1225; DB 14; Length 235;
Best Local Similarity 97.0%; Pred. No. 6.2e-90;
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

Qy 1 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60
Db 4 EPKSCDKTHTCPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 63
Qy 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLTQHWMMNGKEKCKVSNKALPAPIKT 120
Db 64 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLTQHWMMNGKEKCKVSNKALPAPIKT 123
Qy 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180
Db 124 ISKAKGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 183
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181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYQORSLSLSPGK 232  
 184 PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYQORSLSLSPGK 235

35012  
 Sequence 13, Application US/09996357  
 Patent No. US20020133001A1  
 GENERAL INFORMATION:  
 APPLICANT: Gelter, Malcolm L  
 APPLICANT: Isreal, David I  
 APPLICANT: Joyal, John L  
 APPLICANT: Gosselin, Michael  
 TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR  
 TITLE OF INVENTION: TREATING AN AMYLOIDOTIC DISEASE  
 FILE REFERENCE: PPT-105  
 CURRENT APPLICATION NUMBER: US/09/996,357  
 PRIOR FILING DATE: 2001-11-27  
 PRIOR APPLICATION NUMBER: 60/253,302  
 PRIOR FILING DATE: 2000-11-27  
 PRIOR APPLICATION NUMBER: 60/250,198  
 PRIOR FILING DATE: 2000-11-29  
 PRIOR APPLICATION NUMBER: 60/257,186  
 PRIOR FILING DATE: 2000-12-20  
 NUMBER OF SEQ ID NOS: 13  
 SOFTWARE: PatentIn Ver. 2.0  
 SEQ ID NO 13  
 LENGTH: 247  
 TYPE: PRT  
 ORGANISM: Homo sapiens

3-09-996-357-13  
 Query Match 97.2%; Score 1225; DB 9; Length 247;  
 Best Local Similarity 97.0%; Pred. No. 6.6e-90;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
 16 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 75  
 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLIHQWMMNGKEYCKVSNKALPAPIEKT 120  
 76 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLIHQWMMNGKEYCKVSNKALPAPIEKT 135  
 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
 136 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 195  
 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYQORSLSLSPGK 232  
 196 PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYQORSLSLSPGK 247

35013  
 Sequence 18, Application US/10008063  
 Publication No. US20030092164A1  
 GENERAL INFORMATION:  
 APPLICANT: Gross, Jane A.  
 APPLICANT: Xu, Wenfeng  
 APPLICANT: Henne, Randal M.  
 APPLICANT: Grant, Francis, J.  
 TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor  
 FILE REFERENCE: 00-103  
 CURRENT APPLICATION NUMBER: US/10/008,063  
 CURRENT FILING DATE: 2001-11-05  
 NUMBER OF SEQ ID NOS: 46  
 SOFTWARE: PatentIn Ver. 4.0  
 SEQ ID NO 18  
 LENGTH: 251  
 TYPE: PRT  
 ORGANISM: Homo sapiens

3-10-008-063-18  
 Query Match 97.2%; Score 1225; DB 14; Length 251;  
 Best Local Similarity 97.0%; Pred. No. 6.7e-90;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
 20 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 79  
 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLIHQWMMNGKEYCKVSNKALPAPIEKT 120  
 80 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLIHQWMMNGKEYCKVSNKALPAPIEKT 139  
 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
 140 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 199  
 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYQORSLSLSPGK 232  
 200 PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYQORSLSLSPGK 251

US-10-008-063-18  
 Query Match 97.2%; Score 1225; DB 14; Length 251;  
 Best Local Similarity 97.0%; Pred. No. 6.7e-90;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
 20 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 79  
 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLIHQWMMNGKEYCKVSNKALPAPIEKT 120  
 80 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLIHQWMMNGKEYCKVSNKALPAPIEKT 139  
 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
 140 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 199  
 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYQORSLSLSPGK 232  
 200 PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYQORSLSLSPGK 251

RESULT 14  
 US-10-152-363A-6  
 ; Sequence 6, Application US/10152363A  
 ; Publication No. US20030103985A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Rixon, Mark W.  
 ; APPLICANT: Gross, Jane A.  
 ; TITLE OF INVENTION: TACI-Immunoglobulin Fusion Proteins  
 ; FILE REFERENCE: 01-20  
 ; CURRENT APPLICATION NUMBER: US/10/152,363A  
 ; CURRENT FILING DATE: 2002-05-20  
 ; PRIOR APPLICATION NUMBER: 60/293,343  
 ; PRIOR FILING DATE: 2001-05-24  
 ; NUMBER OF SEQ ID NOS: 70  
 ; SOFTWARE: FastSeq for Windows Version 3.0  
 ; SEQ ID NO 6  
 ; LENGTH: 251  
 ; TYPE: PRT  
 ; ORGANISM: Homo Sapiens

US-10-152-363A-6  
 Query Match 97.2%; Score 1225; DB 14; Length 251;  
 Best Local Similarity 97.0%; Pred. No. 6.7e-90;  
 Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;

1 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 60  
 20 EPKSCDKTHTCPPCPAPPELLGGPSVFLFPPKPKDTLMISRTPEVTCVVDVSHEDPEVKF 79  
 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLIHQWMMNGKEYCKVSNKALPAPIEKT 120  
 80 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLIHQWMMNGKEYCKVSNKALPAPIEKT 139  
 121 ISKAKVQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 180  
 140 ISKAKGQPREQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTTTP 199  
 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYQORSLSLSPGK 232  
 200 PVLDSVGSFFLYSKLTVDKSRWQGNVFCVSMHEALHNNHYQORSLSLSPGK 251

RESULT 15  
 US-09-996-357-12  
 ; Sequence 12, Application US/09996357  
 ; Patent No. US20020133001A1  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Gelter, Malcolm L  
 ; APPLICANT: Isreal, David I  
 ; APPLICANT: Joyal, John L

APPLICANT: Gosselin, Michael  
TITLE OF INVENTION: THERAPEUTIC AGENTS AND METHODS OF USE THEREOF FOR  
FILE REFERENCE: PPI-105  
CURRENT APPLICATION NUMBER: US/09/996,357  
CURRENT FILING DATE: 2001-11-27  
PRIOR APPLICATION NUMBER: 60/253,302  
PRIOR FILING DATE: 2000-11-27  
PRIOR APPLICATION NUMBER: 60/250,198  
PRIOR FILING DATE: 2000-11-29  
PRIOR APPLICATION NUMBER: 60/257,186  
PRIOR FILING DATE: 2000-12-20  
NUMBER OF SEQ ID NOS: 13  
SOFTWARE: PatentIn Ver. 2.0  
SEQ ID NO 12  
LENGTH: 267  
TYPE: PRT  
ORGANISM: Artificial Sequence  
FEATURE:  
OTHER INFORMATION: Description of Artificial Sequence:alpha-beta(16-30)Fc  
US-09-996-357-12

Query Match 97.2%; Score 1225; DB 9; Length 267;  
Best Local Similarity 97.0%; Pred. No. 7.2e-90;  
Matches 225; Conservative 3; Mismatches 4; Indels 0; Gaps 0;  
QY 1 EPKSCDKTHTCPPCPAPELIGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 60  
DB 36 EPKSCDKTHTCPPCPAPELIGGPSVFLFPKPKDTLMISRTPEVTCVVVDVSHEDPEVKF 95  
QY 61 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 120  
DB 96 NWYVDGVEVHNKTKPREEQYNSTYRVVSVLTVLHQDWLNGKEYCKVSNKALPAPIEKT 155  
QY 121 ISKAKVQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 180  
DB 156 ISKAGQPREPQVYTLPPSRDELTKNQVSLTCLVKGFYPSDIAVEWESNGQPENNYKTP 215  
QY 181 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 232  
DB 216 PVLDSVGSFFLYSKLTVDKSRWQGNVFSCVMEALHNHYTQKSLSLSPGK 267

Search completed: October 27, 2004, 17:20:19  
Job time : 72.0036 secs